AL187941 Tetraodon Bf630719 HVSMED001 AL064088 Drosophil AL514737 AL514737

ALO64089 Drosophil AQ917446 Drosophil AQ917405 Drosophil ALO2900 T3 end of AQ917102 T233131b ALO69706 Drosophil ALO69706 Drosophil ALO69706 Drosophil ALO6732 Drosophil ALO6732 Drosophil ALO6732 Drosophil ALO6732 Drosophil ALO6732 Drosophil ALO6970 Drosophil ALO6970 Drosophil ALO6970 Drosophil ALO6971 Drosophil ALO6971 Drosophil ALO6972 Drosophil ALO6973 Drosophil ALO6973 Drosophil ALO6973 Drosophil ALO6973 Drosophil ALO6973 Drosophil ALO6973 Drosophil ALO6971 Brosophil ALO6971 Brosophil ALO6971 Drosophil ALO6973 Drosophil

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Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage: Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage: BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billand at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Drosophila melanogaster genome survey sequence T7 end of BAC
BACN044120 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fruit fly.
Plasmid Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/plasmid="pBeloBA111"
/db_xref="taxon:7227"
/clone_lbb="DrosBAC"
/clone="BACN04L20"
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AZ929020
CNS02PW4
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AQ915359
CNS016LI
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AL055440 Drosophil
AQ506817 RPCI-11-2
AQ917446 T233481b
AQ098895 HS_3050_A
AL238491 Tetracdon
AQ745537 HS_2272_A
AL077203 Drosophil
AL077232 Drosophil
AL077865 Drosophil
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AL077865 Drosophil
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Tetraodon
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RPCI-11-2
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                                                                      ; Search time 2253.73 Seconds
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          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                     11351937 seqs, 5372889281 residues
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                                                                      December 19, 2001, 17:00:29
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Maximum Match 100%
Listing first 45 summaries
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CNSOOJG1
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                                                  nucleic search, using sw model
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Perfect score:
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03-JUN-1999

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BASE COUNT ORIGIN

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from Drosophila melanogaster (fruit
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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AL055440. GI:4932241
                       141 caagatgggaattaacatctacaaattgccttttcttatcgaccatgtacatcctaccat
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Best Local Similarity 38.3
Matches 147; Conservative
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk . This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
I (bases 1 to 1101)
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; Pred. No. 0.008;
43; Mismatches 77; Indels 0;
                    171 others
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Best Local Similarity 41.9%; Pred. No. 0.051;
Matches 88; Conservative 38; Mismatches 84;
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/note="end
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DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

RESULT CNS00Z38 LOCUS

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ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

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Web: www.genoscope.cns.fr.

Web: www.genoscope.cns.fr.

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCT-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; on bw sp. the same strain used for the BDGP's pland by the order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://Dacpac.med.buffalo.edu/drosophila_bac.htm.
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                                                                                                                        AQ506817 537 bp DNA GSS 29-APR-1999
RPCI-11-281J17.TV RPCI-11 Homo sapiens genomic clone RPCI-11-281J17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: hbe@tigr.cog
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library availability, please contact Pieter de Jong
(pieter@dejong, med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 537)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /ccll_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIll Human Male BAC Library"
a 11 c 30 g 280 t
                                                                                                                                                                                                                         319 gaacatgattaatgcttgtgagttgttctcatccgtaagagtttcaatatgtaatggtga 378
                                                        taattataattataattatataataatgaaaccatggtgccccctgctgctttacatgga 259
                                                                                        875 ТИААТАТАТТТТТААТАТТАИАТИААТТААНТААНТАААТИТТТАИТАТТТТИТАИТТ 934
                                                                                                                                                                935 TKTTATWTTAWDATWWTATTWATATWTATWTAAAAWWTAAWWTWWAWATTTATATAT 994
Length 537;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
Other GSSs: RPCI-11-281JJ7.TJ
Other GSSs: RPCI-11-281JJ7.TJ
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.4%; Score 55.8; DB 13; ilarity 48.5%; Pred. No. 0.21; Conservative 1; Mismatches 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="GDB:7607752"
/db_xref="taxon:9606"
/clone="RRCI-11-281J17"
/clone_lib="RRCI-11"
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                                                                                                                                                                                                                                                                          379 agagtcaaaacccaaaatcatgaa 402
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AQ506817.1 GI:4711564
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Medicago truncatula
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Trifolleae;
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/clone_lib="Medicago truncatula BAC library"
/note="Vector: paleloBAC11; Site_1: HindIII; Site_2:
/note="Vector: paleloBAC11; Site_1: HindIII; Nam. Y-W, Penmetsa, R.V, Endre, G., Kim, D., an Cook, D.R. 1999. Construction of a bacterial artificial chromosome library of Medicago truncatula and identification of clones containing ethylene response agenes. Theor Appl Genet 98: 638-646. "
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Other name: DK457-L; date: 8/12/99; Submitted to the Database of
Genome Survey Sequences (GSS) on 12/06/99; More information is
available at 'http://chrysie.tamu.edu/medicago'.
Seq primer: SO-BAC-L (AACGCCAGGGTTTTCCCAGTCACGACG)
Class: BAC ends.
                                                                                                                                            141 caagatgggaattaacatctacaaattgccttttcttatcgaccatgtacatcctaccat 200
                                                                                                                                                                                                                                                                           219 ATATATTGATATATATTTATATATTGATATATATATTGATATATGTATATATATATATAT 278
                                                                                                                                                                                                                                                                                                                                 201 aattataattataattatatataatactgaaaccatggtgccccctgctgctttacatggat 260
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Contact: Cook DR
The Crop Biotechnology Center
Texas A&W University
Department of Plant Pathology and Microbiology, Rm 120
Peterson Bildy, College Station, TX 77843-2132, USA
Tel: 409 862 4790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kim,D., Limpens,E., Peng,H., Ellis,L. and Cook,D.R.
BAC end sequencing of Medicago truncatula
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSS
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/organism="Medicago truncatula"
/cullivar="genctype A17"
/db_xref="taxon:3880"
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CNS03D0I 844 bp DNA GSS 15-MAY-2000
Tetraodon nigroviridis genome survey sequence PUC-ori end of clone
015L14 of library G from Tetraodon nigroviridis, genomic survey
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Tetracdom nigroviridis

Tetracdom nigroviridis

Tetracdom nigroviridis

Tetracodom nigroviridis

Tetracodom nigroviridis

Actinopterygii; Teleostei; Euteleostei; Neoteleostei;

Actinopterygii; Teleostei; Euteleostei; Neoteleostei;

Tetracodontidae; Tetracodom.

Tetrac
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Tetraodon nigroviridis DNA sequence
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Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
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This sequence is a single read and was generated as part of a lar
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                          93 atacotgacttgttatttatcaataaatatttaaactatattctttcaagatgggaat 152
                                                                                                                                                                                                                                                                         153 taacatctacaaattgccttttcttatcgaccatgtacatcctaccataattatat 212
                                                                                                                                                                                                                                                                                                                                                                                                                         aattatataatactgaaaccatggtgccccctgctgctttacatggatttctccgctact 272
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                          75
                                                                                                                        33 attgaaatatttctgaatttaaacttgcatcaataaawttatgttttgcttggactata
                                                                                                                                                                     /clone_lib="G"
/^note="Genoscope sequence ID : C0BG015DF07SPl~end
PUC-Or"
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                                            Length 300;
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Pred. No. 0.28;
1; Mismatches 142;
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.Coganism-Tetraodon nigroviridis"
./db.xref-"taxon:99883"
/clone="015514"
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                                  13.3%;
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1 (bases 1 to 300)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQ098895 300 bp DNA GSS 27-AUG-1998
8-23050_A1_C03_MR CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3050 Col=5 Row=E, DNA sequence.
AQ098895
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/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
                                                                                                                                                                                               201 aattataattataattatatataatactgaaaccatggtgccccctgctgcttacatggat 260
                                                                    Gaps
                                                                                           21 atataatcagttattgaaatatttctgaatttaaacttgcatcaataaawttatgttttt 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
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                  Length 421;
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High Throughput Sequencing Center
Holyversity of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3818
Emax: (206) 616-3887
Emal:: yallace@u.washington.edu
                                                               Indels
             Score 55.6; DB 13;
Pred. No. 0.24;
1; Mismatches 165;
          Score 55.6;
Pred. No. 0.
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/db_xref="taxon:9606"
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Location/Qualifiers
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Class: BAC ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          321 acatgattaatgcttgtgag 340
       13.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQ745537 845 bp DNA GSS 16-JUL-1999 HS_2272_A2_B12_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2272 Col=24 Row=C, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 2272 row: C column: 24
Seg primer: T7
Class: BAC ends
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                                                                                                           218 TTTTTAFKTGTATATTTTTTTTTTTTTTTTTTAATKTTTTTTWTTTTATCATTTAK 277
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               Length 844;
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High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109,
                                          7; Mismatches 170;
             Score 55.2; DB 13;
Pred. No. 0.26;
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/db_xref="taxon:9606"
/clone="Plate=2272 Col=24 Row=C"
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153; Conservative
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B 191 91006 EVRY cedex - FRANCE (E-mail: seqrefgenoscope.cns.fr

Web: www.genoscope.cns.fr)

Petermination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the 1sogenic strain y2; cn bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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BACR39E17 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
AL077203
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Pteryyota, Neoptera, Endopteryyota, Diptera, Brachycera,
Muscomorpha, Ephydroidea, Drosophilldae, Drosophila.
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     Length 845;
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/db_xref="taxon:7227"
/clone_lib="RPC1-98"
/clone="BACR39E17"
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Score 55.2; DB 13;
Pred. No. 0.26;
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- Web : www.genoscope.cns.fr |
- Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila please see http://www.frutifly.org The BDGP Drosophila please see http://www.frutifly.org The BDGP Drosophila halanogaster BAC ilbrary was prepared by Kazutoyo Oscogawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, Korg I dispation of Drosophila Dark Cancer Institute in Buffalo, ECORI dispation of Drosophila Dark Cancer Institute in Buffalo, ECORI dispation of Drosophila Dark Cancer Institute in Buffalo, BT and EST libraries. A more detailed description of the library fluters for hybridization from the BACPAC Resource Center can be Location/Quallifers form the BACPAC Resource Center.
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Drosophila melanogaster genome survey sequence T7 end of BAC:
### BACR30J18 of RPCI-98 library from Drosophila melanogaster (fruit
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                                                                          Length 1101;
            126 others
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Pred. No. 0.25;
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/db_xref="taxon:7227"
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            489
          73 g
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13.3%;
Best Local Similarity 42.1%;
Matches 144; Conservative
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ALE SUBMITTEED (102-10W-1999) Genoscope - Centre National de Sequencage :
- Web 194 19006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Epiydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 928)
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                                                                                                                                                                                                                        Length 980;
                                                                                                  69 others
                                                                                                                                                                                                  Query Match
13.2%; Score 55; DB 13; Le
Best Local Similarity 41.9%; Pred. No. 0.27;
Matches 142; Conservative 37; Mismatches 155;
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/clone_lib="RPCI-98"
/clone="BACR38J18"
/note="end : T7"
a 112 c 102 g
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage:
Bp 191 91006 EVRz cedex - FRANCE (E-mail: seqref@genoscope.cns.fr

Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA pare Strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     145 atgggaattaacatctacaaattgccttttcttatcgaccatgtacatcctaccataatt 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       205 ataattataattataataatactgaaaccatggtgccccctgctgcttacatggatttct 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    265 ccgctactatttgtatacgtgtatatataccgtataatgtacatatatttatatgaacat 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           616 АИИАААТАТИТИАТАТАТАТАТИТИТИТИТИТИТИТАТАТАТАИАААИААААИАА
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 980)
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                                                                                                                                                                                 Length 928;
                                                                                                     191 others
/organism="Drosophila melanogaster"
/db_xref="Laxon:7227"
/clone_lib="RPCI-98"
/clone="BACR27A24"
                                                                                                                                                                                                                            69; Mismatches 141;
                                                                                                                                                                                       DB 13;
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                                                                                                                                                                                   Score 54.8; Dl
Pred. No. 0.3;
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                                                                                                     84 g
                                                                               /note="end : T7"
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Drosophila melanogaster
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31.4%;
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Best Local Similarity
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NSOOJG1/c
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Libert Submission of the Sequence of Sequence of Submisted (02-JUN-1999) Genoscope - Centre National de Sequencege:

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)

Determination of this BAC-ed sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 ttgaaatatttctgaatttaaacttgcatcaataaawttatgtttttgcttggactataa 93
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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                                                             melanogaster"
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13.2%; Score 54.8; DB 13;
Best Local Similarity 43.6%; Pred. No. 0.3;
Matches 129; Conservative 22; Mismatches 145;
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                                                                                                                                                                                                                      297
                                                  /organism="Drosophila m
/db_xref="taxon:727"
/clone=lib="krec198"
/clone="BACR38118"
/note="end : T?"
Location/Qualifiers
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Drosophila melanogaster
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GSS: genome higher variation in the control of the control o
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genomic survey
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Tetraodon nigroviridis genome survey sequence T7 end
249F10 of library G from Tetraodon nigroviridis, geno
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            melanogaster"
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Pred. No. 0.32;
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/organism="Drosophila me/db_xref="taxon:727"
/clone_lib="RPCI-98"
/clone="BACR29B23"
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llarity 34.3%; Pre
Conservative 70;
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Matches 128;
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Best Local
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ORIGIN
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Direct Submission
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This Sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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                                                                                                                                                                                                     ID : COAG249DC05LP1~end : T7"
t 119 others
                                                                                                                                                                                                                                                                                                                                                                                             355 WWADKRATTAGGGTTTTWAAAAWWWWTTTTAATTCAAAGGGTTTATWWWTWWTATT 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wing R., Close T.J., Kleinhofs A., Wise R., Begum D., Frisch D., Yu Y. Anderson H., Dale J., Henry D., Kernodle S., Palmer M., Rambo T., Saski C., Schwartzbeck J., Simmons J., Choi D.W., Main D., Wood T., "Development of a genetically and physically anchored EST resource for barley genomics";
                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          149 gaattaacatctacaaattgccttttcttatcgaccatgtacatcctaccataattataa 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                415 GACTAWTAAWWITTAANNTANAWNGTTTTWWNTTTWAWAATATAAWATWTWTAT 474
                                                                                                                                                                                                                                                                                                                                 29 agttattgaaatatttctgaatttaaacttgcatcaataaawttatgtttttgcttggac 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HVSMEb0013H16f Hordeum vulgare seedling shoot EST library HVcDNA0002 (Dehydration stress) Hordeum vulgare cDNA clone HVSMEb0013H16f, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiolantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae;
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                    Length 678;
                                                                                                                                                                                                                                                                                                                Indels
                                                                                                         1..678
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="24970"
/clone=11b="G"
/note="Genoscope sequence ID : COAG;
/note="Genoscope sequence ID : COAG;
                                                                                                                                                                                                                                                                          13.1%; Score 54.4; DB 13; 37.2%; Pred. No. 0.38; 1ve 44; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209 ttataattataataatactgaaaccatggtgcccctgc 246
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST; 1337
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21-DEC-2000 (Rel. 66, Last upd
                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; RNA;
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                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity
....nes 81; Conserva
                                                                                                                                                                                                              126
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ij
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HVCDNA002 [DAGATATION STRESS]"
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                                                                                                                   /db_xref="taxon:4513"
/note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xhol"
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                                                                                                                                                                                                                                                                                                                                                                                                                                         1027 TITATITGITTITTATTCATATITGATATATTATTATTATTATTACTATATTGI 1086
                                                                                                                                                                                                                                                                                                                            158 tctacaaattgccttttcttatcgaccatgtacatcctaccataattataatta 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          210 tataatactgaaaccatggtgcccctgctgctttacatggatttctccgctactatttg 277
                                                                                                                                                                                                                                                                                                        4;
                                                                                                                                                                                                                                                                               Length 1337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 12.9%; Score 53.8; DB 5; Length 1 Best Local Similarity 51.2%; Pred. No. 0.44; Matches 147; Conservative 1; Mismatches 135; Indels
                                                                                                                                                                                                                                            Sequence 1337 BP; 292 A; 22 C; 74 G; 941 T; 8 other;
                                                                                  Location/Qualifiers
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: AATACCCTCACTAAAGGG
High quality sequence start: 38
High quality sequence stop: 1204.
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                                                                                                          source
                                                                                  Key
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Search completed: December 19, 2001, 17:00:33 Job time: 2275 sec

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1303 17 AAT39337 Plasmid pTS88 (Eco 3201 12 AAQ14529 Pt ICP codi 4832 22 AAH25423 Nucleotide sequenc 4946 18 AAT95931 T-DNA of plasmid p 4946 18 AAT95422 Nucleotide sequenc 5349 19 AAV32239 T-DNA of pTTS24 T-DNA of pTTS24 T-DNA of pTTS24 T-DNA of pTTS24 T-DNA Of DTTS24 T-DNA OF DTASMIG DTDS84 CON 7639 14 AAQ42160 Plasmid pJD884 CON	1037 11 AAQ04705 USP-Prc 1105 11 AAQ04703 USP-Prc 1106 11 AAQ04706 USP-SI AAQ04706 USP-SI AAQ04706 USP-SI AAQ05139 USP-SI AAQ05121 AAZ29121 AAZ29124 Plasmid 3877 21 AAZ29123 Plasmid 3877 21 AAZ99123 Plasmid 3877 21 AAZ99123	24593 6 AAN50226 24596 6 AAN50182 936 22 AAF58252 936 22 AAF58257 936 22 AAF58259 936 22 AAF58262 938 22 AAF58262	936 22 AAF58252 Oligon 936 22 AAF58254 Oligon 936 22 AAF58259 Oligon 936 22 AAF58259 Oligon 936 22 AAF58262 Oligon 938 22 AAF58255 Oligon ALIGNMENTS	dard; DNA; 416 BP. (first entry) der flanking region of elite event MS-B2. vent; transgenic Brassica plant; transformation event; y gene; ds.	um sp. on/Qualifiers a "Corresponds to T-DNA" 16	/note= "Corresponds to plant DNA" 1042-A2. 2001. 2000; 2000WO-EP10680. 1999; 99US-0430497. AVENTIS CROPSCIENCE NV.
12 189.6 13 189.6 14 189.6 15 189.6 17 189.6 17 189.6 189.6 189.6 20 189.6 21 189.6	22 183.6 4 22 183.6 4 22 183.6 4 22 17.9 4 22 17.9 28 145.6 3 3 1145.6 3 3 1145.6 3 3 1145.6 3 3 1145.6 3	32 145.6 3 34 104.6 2 35 104.6 2 37 104.6 2 37 104.6 2 38 104.6 2 39 104.6 2	104.2 104.2 104.2 104.2 104.2 2 2 2	SULT 1 20699 AAD06999 standa AAD06999; 06-AUG-2001 (f Left (3') borde MS-B2 ellte eve male-sterility	Chimeric - Agro Chimeric - Bras Key misc_feature misc_feature	XX XX
n 4.5 Compugen Ltd. ; Search time 230.16 Seconds (without alignments) 1549.562 Million cell updates/sec	catgaac	meters: 1861242	geneseq/geneseqn/NA1980.DAT:* geneseq/geneseqn/NA1981.DAT:* geneseq/geneseqn/NA1982.DAT:* geneseq/geneseqn/NA1983.DAT:* geneseq/geneseqn/NA1984.DAT:* geneseq/geneseqn/NA1985.DAT:* geneseq/geneseqn/NA1985.DAT:*	cgdata/geneseq/geneseqn/NA1988.DAT:* /gcgdata/geneseq/geneseqn/NA1989.DAT:* /gcgdata/geneseqn/NA1999.DAT:* /gcgdata/geneseqn/NA1991.DAT:* /gcgdata/geneseqn/NA1991.DAT:* /gcgdata/geneseqn/NA1991.DAT:* /gcgdata/geneseqn/NA1993.DAT:* /gcgdata/geneseqn/NA1994.DAT:* /gcgdata/geneseqn/NA1995.DAT:* /gcgdata/geneseqn/NA1995.DAT:* /gcgdata/geneseqn/NA1995.DAT:* /gcgdata/geneseqn/NA1995.DAT:* /gcgdata/geneseqn/NA1999.DAT:* /gcgdata/geneseqn/NA1999.DAT:* /gcgdata/geneseqn/NA1999.DAT:* /gcgdata/geneseqn/NA1999.DAT:* /gcgdata/geneseqn/NA1999.DAT:* /gcgdata/geneseqn/NA1999.DAT:*	results predicted by chance to have a lot the score of the result being printed, of the total score distribution. SUMMARIES ID	Left (3') border Fright (5') border Plasmid pTC0113 T-Chimeric T-DNA of Nucleotide sequence Plasmid pTS172delt E. coli plasmid pTS174 use Plasmid pTS172. C. E. coli plasmid pTS172. C. E. coli plasmid pTS174 use Plasmid pTS172. C. E. coli plasmid pTS174 use Plasmid pTS346. U
GenCore version Copyright (c) 1993 - 2000 : - nucleic search, using sw model December 19, 2001, 17:31:51	us-09-698-903B- 416 1 ctacggcaatgta e: IDENTITY_NUC Gapop 10.0 , Ga	umber of hits satisfying chosen parameters DB seq length: 0 DB seq length: 2000000000 Ocessing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	_ - - - - - - - - - - - - - - - - - - -	9: SIDSB/gcgdata/geneseq/geneseqn/NA198B.DAT:* 10: SIDSB/gcgdata/geneseq/geneseqn/NA198B.DAT:* 11: SIDSB/gcgdata/geneseq/geneseqn/NA199D.DAT:* 12: SIDSB/gcgdata/geneseq/geneseqn/NA199D.DAT:* 13: SIDSB/gcgdata/geneseq/geneseqn/NA1992.DAT:* 14: SIDSB/gcgdata/geneseq/geneseqn/NA1992.DAT:* 15: SIDSB/gcgdata/geneseq/geneseqn/NA1992.DAT:* 16: SIDSB/gcgdata/geneseq/geneseqn/NA1995.DAT:* 17: SIDSB/gcgdata/geneseq/geneseqn/NA1995.DAT:* 18: SIDSB/gcgdata/geneseq/geneseqn/NA1995.DAT:* 19: SIDSB/gcgdata/geneseq/geneseqn/NA1996.DAT:* 20: SIDSB/gcgdata/geneseq/geneseqn/NA1999.DAT:* 21: SIDSB/gcgdata/geneseq/geneseqn/NA1999.DAT:* 22: SIDSB/gcgdata/geneseq/geneseqn/NA1999.DAT:* 22: SIDSB/gcgdata/geneseq/geneseqn/NA2000.DAT:*	No. is the number of greater than or equal; derived by analysis Query Ouery The Match Length DB	415.6 99.9 416 22 AAD06999 180.8 91.5 46.3 5864 17 AAT39339 192.6 46.3 5864 17 AAT39339 192.6 46.3 5865 22 AAD06990 190 45.7 5228 22 AAF86439 190 45.7 6548 17 AAT39336 190 45.7 6548 18 AAT61394 190 45.7 6548 21 AAT61394 190 45.7 6548 21 AAT61394 190 45.7 7492 22 AAF86441
QM nuc eic	: Q G G G	Total number Minimum DB s Maximum DB s Post-process	Databage :		red. core nd is nd is Result	0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

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                                                                                              The present invention relates to a transgenic Brassica plant or its seed, cells or tissues, characterised by harbouring a specific transformation event, particularly by the presence of a male-sterility gene, at a specific location in the Brassica genome. Transgenic transgenic transgenic plant with a male-fertile Brassica plant and harvesting the hybrid seed from the transgenic Brassica plant.

The present sequence is left (3') border flanking region of elite event MS-B2.
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m of}^{
m by}
                                                                                                                                                                                                                                                                                                                                           61 atcaataaawttatgtttttgcttggactataatacctgacttgttattttatcaataaa 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                           coctgotgotttacatggatttctccgctactatttgtatacgtgtatataccgtata 300
                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                1 ctacggcaatgtaccagctgatataatcagttattgaaatatttctgaatttaaacttgc 60
                                                                                                                                                                                                                                                                         Transgenic Brassica plants, seeds, cells or tissues, characterized harboring specific transformation events, particularly by presence male-sterility gene, at specific location in its genome -
                                                                                                                                                                                                                                                                                                                elite event; transgenic Brassica plant; transformation event;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                 Length 416;
                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Right (5') border flanking region of elite event MS-B2.
                                                                                                                                                                                           Sequence 416 BP; 137 A; 72 C; 54 G; 152 T; 1 other;
                                                                                                                                                                                                                            99.9%; Score 415.6; DB 22;
100.0%; Pred. No. 1.6e-74;
1ve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                           Claim 11; Page 52; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD06997 standard; DNA; 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric - Agrobacterium sp. Chimeric - Brassica sp.
   De Beuckeleer
                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 416; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         male-sterility gene; ds.
                   WPI; 2001-300517/31
  Weston B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-AUG-2001
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The present invention relates to a transgenic Brassica plant or its seed, cells or tissues, characterised by harbouring a specific transformation event, particularly by the presence of a male-sterility gene, at a specific location in the Brassica genome. Transgenic Brassica plant is useful for producing a hybrid seed by crossing the transgenic plant with a male-fertile Brassica plant and harvesting the hybrid seed from the transgenic Brassica plant.
                                                                                                                                                                                                                                      bγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                            Transgenic Brassica plants, seeds, cells or tissues, characterized harboring specific transformation events, particularly by presence male-sterility gene, at specific location in its genome -
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 415;
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Pred, No. 1.4e-67;
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 415 BP; 154 A; 55 C; 70 G; 136 T; 0 other;
  1..234
//rtag= a
//note= "Corresponds to plant DNA"
235..415
                                             /*tag= b
/note= "Corresponds to T-DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                     Claim 11; Page 51; 53pp; English.
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                                                                                                                                                               (AVET ) AVENTIS CROPSCIENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                    91.5%;
98.5%;
                                                                                                                     26-OCT-2000; 2000WO-EP10680
                                                                                                                                            99US-0430497
                                                                                                                                                                                   Weston B, De Beuckeleer M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       404; Conservative
                                                                                                                                                                                                        WPI; 2001-300517/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                           WO200131042-A2
                                                                                                                                         29-OCT-1999;
                                  misc_feature
                                                                                                 03-MAY-2001
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Best Local S
Matches 404
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96WO-EP00722

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RESULT
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                                                                                                                                                                                                                                                                                                               /note= "region containing polyA signal of nopaline synthase gene of Agrobacterium T-DNA" complement (3032..3367)
                                                                                                                                                                                                                                                                                                                                                         /note= "Bacillus amyloliquefaciens barnase coding
                                                                                                                                                                                                                                                                                                                                                                                                   of
                                                             Plasmid pTC0113 T-DNA used to obtain male sterile oilseed rape.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
                                                                                                                                                                                         gene
                                                                             Plasmid pTCO113; male sterile; barnase; ribonuclease; barstar; transgenic plant; oilssed rape; canole; Brassica napus; ds.
                                                                                                                                                                                                                                                                                                                                                                                /*tag= g
/label= PTA29
/note= "promoter of stamen-specific TA29 gene
Nicotiana tabacum"
                                                                                                                                                                                                                                                                      /note= "promoter of Arabidopsis Rubisco small
subunit gene"
complement (2659..3031)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "region coding for barstar of Bacillus amyloliquefaciens"
                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "promoter of nopaline synthase gene of Agrobacterium T-DNA"
                                                                                                                                                     /note= "right border of Agrobacterium T-DNA" complement (98..330)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= k
/label= LB
/note= "left border of Agrobacterium T-DNA"
                                                                                                                                                                                                                              /notes "region coding for phosphinothricin
acetyltransferase"
complement (883..2608)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= j
/label- 3'g7
/note= "region containing polyA signal of
of Agrobacterium T-DNA"
complement (5840..5864)
                                                                                                                                                                                      /note- "region containing polyA signal of of Agrobacterium T-DNA" complement (331..882)
                                                                                                                                                                                                                                                                                                                                                                  region"
complement (3368..4877)
                                                                                                                      Location/Qualifiers complement (1..25)
               AAT39339 standard; DNA; 5864 BP.
                                                                                                                                                                                                                                                                                                                                           /*tag= f
/label= Barnase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label- Barstar
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/label= 3'nos
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/label= Pssu
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/label= 3'97
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/label= Pnos
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/label= bar
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                                              (first entry)
                                                                                                                              misc_feature
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                                                                                                                                                                polyA_signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9626283-A1
                                              22-JAN-1997
                                                                                                      Synthetic
                              AAT39339,
                                                                                                                                                                                                                                                promoter
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29-AUG-1996

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T-DNA; plasmid pTCO113; transgenic Brassica plant; transformation event; male-sterility gene; chimeric; tobacco; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 tatttaaactatatttctttcaagatgggaattaacatctacaaattgccttttcttatc 180
                                                                                                                                                                                                                                                                                                                  plasmid pTCO113 (AAT39339) is a T-DNA vector containing a bar gene under control of the PSSU promoter, a barnase gene under control of the stamen-specific PTA29 promoter, and a barstar (co-regulatory) gene under control of the Pnos promoter. 87% of oilseed rape plants regenerated after Agrobacterium-mediated transformation using pTCO113 were male sterile. Barnase expression disturbed the function of stamen cells leading to male sterility. Constitutive expression of barstar counteracted any low level expression of barnase in non-stamen tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ctacggcaatgtaccagctgatataatcagttattgaaatattctgaatttaaacttgc 60
                                                                                                                                                                 Prodn. of male sterile plants by transforming with a chimaeric construct - comprising a male sterility DNA e.g. barnase and a co-regulating gene, e.g. barstar, into the nuclear genome, useful for generating hybrid cultivars
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46.3%; Score 192.6; DB 17; Length 5864; 99.5%; Pred. No. 4.6e-30; Artive 1; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5864 BP; 1849 A; 1094 C; 1150 G; 1771 T; 0 other;
                                                                                                                                                                                                                                                                            Example 3; Page 33-3743-47; 56pp; English.
                                                                                  Ē
                                                                                  Michiels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric - Streptomyces hygroscopicus.
Chimeric - Arabidopsis thaliana.
Chimeric - Bacillus amyloliquefaciens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric - Nicotiana tabacum.
Chimeric - Agrobacterium tumefaciens.
Chimeric - Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                        GENETIC SYSTEMS
                                                                                  Cornelissen M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD06990 standard; DNA; 5865
95EP-0400364
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Best Local Similarity 99.5'
Matches 192; Conservative
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                                                                                                                             WPI; 1996-402373/40.
                                        (PLBZ ) PLANT
                                                                                    Botterman J,
21-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-AUG-2001
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The present invention relates to a transgenic Brassica plant or its seed cells or tissues, characterised by harbouring a specific seed cells or tissues, characterised by harbouring a specific transformation event, particularly by the presence of a male-sterility gene, at a specific location in the Brassica genome. Transgenic Transgenic Location in the Brassica genome. Transgenic plant with a male-fertile Brassica plant and harvesting the transgenic Brassica plant and harvesting the comprises right border repeat. T-DNA of plasmid prooll3. This sequence region (UTR) from TL-DNA of PribGS3, synthetic polylinker sequence region (UTR) from TL-DNA of PribGS3, synthetic polylinker sequences. Streptomyces hygroscopicus, barnase gene (bar) from and barsetar gene from Bacillus amyloliquefaciens and barsetar gene from Bacillus amyloliquefaciens and barsetar gene from Bacillus amyloliquefaciens and barsetar shalland, the anther-specific gene TA29 from Nicotiana tabacum and nopaline synthase gene from the T-DNA of Prim37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transgenic Brassica plants, seeds, cells or tissues, characterized by harboring specific transformation events, particularly by presence of male-sterility gene, at specific location in its genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ctacggcaatgtaccagctgatataatcagttattgaaatatttctgaatttaaacttgc
                                                                                                                                                                                                             /*tag= x
/note= "Left border repeat from the TL-DNA from
pT1B6S3"
                                                    /*tag= u
/note= "Synthetic polylinker derived sequence"
5774..5810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22; Length 5865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5865 BP; 1849 A; 1095 C; 1149 G; 1772 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
46.3%; Score 192.6; DB 2
Best Local Similarity 99.5%; Pred. No. 4.6e-30;
Matches 192; Conservative 1; Mismatches 0
                       gene 7 (3'g7) of prim6s3"
5767..5773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 47-49; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                    (AVET ) AVENTIS CROPSCIENCE NV.
                                                                                                                                                                                                                                                                                                                                        26-OCT-2000; 2000WO-EP10680
                                                                                                                                                                                                                                                                                                                                                                                                                                       De Beuckeleer M;
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                                   misc_feature
                                                                                   misc_feature
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                                                                                                                                                                                                                                                                                                         03-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                      Weston B,
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/note= "TagI fragment from the 3' untranslated end of the
nopaline synthase gene (3'nos) from the T-DNA of prim37
and containing plant polyadenylation signals"
                                                                                                                                                                                                                                                                                                                                                                       /*tag= g
/note= "Promoter from the atSlA ribulose-1,5-biphosphate
carboxylase small subunit gene from Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= o /*tag= o /*tag= o /*tag= o /*tag= o /*tag= o /*note= "Promoter of the nopaline synthase gene from the 5216..5217 of Agrobacterium tumefaciens" fate..5217 /*tag= p //*tag= p //*tag= "Synthetic polylinker derived sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= k
//note= "The 3' untranslated region downstream from the
Darnase coding sequence of Bacillus amyloliquefaciens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= m
/note= "Promoter region of the anther-specific gene
1829 from Nicotiana tabacum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the
                                                                                                                                                                                                                                                                                                                         by bialaphos resistance hygroscopicus"
1..25
//oteg- a
//noteg- "Right border repeat from the TL-DNA from
p_118653"
                                                                                                                            /*tag= c
/note= "Residual sequence from the TL-DNA at the
iight border repeat"
                                                                                                                                                                   /*tag= d
/note= "The 3' untranslated end from the TL-DNA
310..331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "Protein encoded by barnase gene from Bacillus amyloliquefaciens"
/*tag= m
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/note= "Synthetic polylinker derived sequence"
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/note= "Synthetic polylinker derived sequence"
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/note= "Synthetic polylinker derived sequence"
2660..2920
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2937.3032
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/note= "The 3' untranslated end from the TL-DNA
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/note= "Synthetic polylinker derived sequence"
4925..5215
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/note= "Sequence from the 3' untranslated end
barstar gene from Bacillus amyloliquefaciens"
5531..5554
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//orte- "Synthetic polylinker derived sequence"
5555..5766
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/product= "Protein encoded by barstar gene of
Bacillus amyloliquefaciens"
5491..5530
                                                                                                                                                                                                                                                                                                                    /product= "Protein encoded
gene (bar) of Streptomyces
884..2609
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332..883
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misc_feature
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3'UTR

CDS

promoter

CDS

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3'UTR

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                                                                                                                                                     Plant promoter; root cell; root-specific expression; parasite resistance; nematode resistance; fungal resistance; water stress; salt stress;
                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a plasmid PGKB5. The plasmid contains a plant promoter that directs expression of a selected sequence in root cells at all stages of development of a plant. The plant promoter is used to control expression of genes in a root-specific manner, especially genes that provide resistance to parasites, pests (nematodes or fungi), water and salt stress, or alter sugar content or nitrogen transport. Fragments of the promoter are useful as probes or primers to detect or amplify at least part of the promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New constitutive plant promoter active specifically in roots, useful for controlling expression of pest or drought resistance genes, and related transgenic plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 7599;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 46.3%; Score 192.6; DB 22; Length Best Local Similarity 99.5%; Pred. No. 4.6e-30; Matches 192; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                              (INRG ) INRA INST NAT RECH AGRONOMIQUE.
                                                                                                                                 Nucleotide sequence of a plasmid PGKB5
                                                                                                                                                                         sugar content; nitrogen transport; ss
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                                                                                                                                                                                                                                                                                                                  Pelletier
                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 9; 92pp; French.
                                                                     AAF25320 standard; DNA; 7599 BP
                                                                                                                                                                                                                                                       2000WO-FR01768
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                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                  Mollier P,
                     5801 gaccatgtacatc 5813
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                                                                                                                                                                                                               WO200100833-A1
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                                                                                                             30-APR-2001
                                                                                                                                                                                                                                                                                                                  Hoffmann B,
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                                                                                                                                                                                            Synthetic
                                                                                          AAF25320;
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                                                            AAF25320
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The present invention relates to a method for producing male sterile plants. The method comprises inserting a promoter fragment upstream of an RNAse gene and a second promoter, upstream of an RNAse inhibitor protein gene and inserting it into the plant genome. The method is useful for producing male sterile tobacco, lettuce and rapeseed plants, but preferably rice and maize. The present sequence is a vector used in the method of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Method for producing male sterile rice and maize by inserting RNAse gene and RNAse inhibitor genes with promoters into the plant genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                             Male sterile plant; RNAase inhibitor; plasmid prS172delta; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45.7%; Score 190; DB 22; 99.0%; Pred. No. 1.5e-29; tive 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 14-17; 29pp; Japanese.
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  BP.
AAF86439 standard; DNA; 5228
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                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                (NISB ) JAPAN TOBACCO
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                                                                                                                                  Plasmid pTS172delta
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                                                                                                                                                                                                                         Unidentified
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rice; Oryza
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                                                                                                                                                                                                             Mutate barnase gene for efficient construction of plant transformants, particularly male sterile plants free from any undesirable characters by specifically expressing the gene alone in anther
                                                                                                                                                                                                                                                                                                                                                                                                                                                      6342 ctacggcaatgtaccagctgatataatcagttattgaaatatttctgaatttaaacttgc 6401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmid pTS174; male sterile; barnase; ribonuclease; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           atcaataaawttatgtttttgcttggactataatacctgacttgttattttatcaataaa 120
                                                                                                                                                                                                                                                                    The invention relates to the generation of male sterile plants by the introduction of a mutant barnase gene (AAZ91095) for expression appecifically in the anther of a plant. This sequence represents the E. coll/Agrobacterium shuttle vector plasmid pTS172 which contains the mutated barnase gene (AAZ91095) under control of the cauliflower mosaic virus 355 promoter. The vector also contains a region of the Agrobacterium T-DNA gene 7. The vector is used for transmitting the barnase gene to plants via an Agrobacterium tumefaciens host cell. The transformed plant is used in plant breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tatttaaactatatttctttcaagatgggaattaacatctacaaattgccttttcttatc 180
                            Male sterile plant; mutant barnase gene; anther-specific expression; low fidelity PCR; primer; plant breeding; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ctacggcaatgtaccagctgatataatcagttattgaaatatttctgaatttaaacttgc 60
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                                                                                                                                                                                                                                                                                                                                                                                                     Length 6539;
                                                                                                                                                                                                                                                                                                                                                                  Sequence 6539 BP; 1755 A; 1578 C; 1519 G; 1687 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
         coli plasmid pTS431 containing mutant barnase gene.
                                                                                                                                                                                                                                                                                                                                                                                                  Score 190; DB 21;
Pred. No. 1.5e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmid pTS174 used to obtain male sterile rice.
                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                 Example 3; Page 23-27; 30pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT39336 standard; DNA; 6548 BP.
                                                                                                                                     98JP-0220060.
                                                                                                                  99WO-JP04167
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 99.0%;
Matches 190; Conservative
                                                                                                                                                       (NISB ) JAPAN TOBACCO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                          Nakakido F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 gaccatgtacat 192
                                                                                                                                                                                           WPI; 2000-195581/17.
                                                                            WO200008176-A1.
                                                                                                               03-AUG-1999;
                                                                                                                                    04-AUG-1998;
                                                                                             17-FEB-2000
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                                                                                                                                                                         Hamada K,
                                                         Synthetic
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Plasmid pTS174 (AAT39336) contains Bacillus barnase DNA under control of the stamen-specific PEI promoter. Embryogenic callus from rice vv. Kochihibiki was transformed with pTS174 alone or with pTS88 (see also AAT39337), a plasmid contg. barstar DNA under control of a 15S promoter. With pTS174 alone, I male sterile line was recovered from 48 electroporation cuvettees. With both plasmids, 7 normal male sterile lines were recovered from 40 cuvettes. Barnase expression disturbed the function of stamen cells leading to male sterility. Constitutive expression of barstar counteracted any low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cauliflower mosaic virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /function= region containing polyadenylation signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prodn. of male sterile plants by transforming with a chimaeric construct - comprising a male sterility DNA e.g. barnase and a co-regulating gene, e.g. barstar, into the nuclear genome, useful for generating hybrid cultivars
                                                                                                                                                                                                                                            polyadenylation signa
gene of Agrobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /function= promoter of the stamen-specific El
                                                                                                                                                                                                                                                                                                                                                                                       /product= Bacillus amyloliquefaciens barnase complement (2625..4313)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phosphinothricin acetyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6548 BP; 1757 A; 1578 C; 1523 G; 1690 T; 0 other;
                                                                                        /*tag= a
//label= Vector
/note= "pUC19 derived vector sequences'
complement (2019..2283)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expression of barnase in non-stamen tissue.
                                                                                                                                                                                                                                       /note= "region containing
nopaline synthase
T-DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           promoter of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cornelissen M, Michiels F;
                                                                                                                                                                                                                                                                                                                complement (2284..2624)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 33-37; 56pp; English.
                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= e
/label= P35S
/function= 35S p
5711..6262
                                                                                                                                                                                                                                                                                                                                            /*tag= c
/label= Barnase
                                                                                                                                                                                                                      /label= 3'nos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENETIC SYSTEMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= g
/label= 3'g7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= f
/label= bar
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= PE1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96WO-EP00722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product- p
6263..6496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4336..5710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95EP-0400364
                                                                           2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1996-402373/40.
                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PLBZ ) PLANT
                                                                                                                                                                      polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9626283-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Botterman J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-AUG-1996
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                           promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  promoter
                                               Key
                                                                                                                                                                                                                                                                                                              CDS
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Length 6548;

DB 17;

45.7%; Score 190;

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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                               AAZ91096;
                                                                                                                                                                                                                                                                                                                                                                                                   70
                                                                                                                                                                                                                                                                                                                                                                                                          AAZ91096
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                                                                 6470
                                                                             61 atcaataaawttatgtttttgcttggactataatacctgacttgttattttatcaataaa 120
         Gaps
                                                          1 ctacggcaatgtaccagctgatataatcagttattgaaatatttctgaatttaaacttgc
                                                                                                                                                                                                                                                                                                                                                                                                                /note= "35S promoter region of cauliflower mosaic virus"
                                                                                                                                                                                                                                                                                                                  /note= "3' untranslated region contg. the poly-A signal of Agrobacterium T-DNA nopaline synthase gene" complement (2289..2624)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13' untranslated region contg. the poly-A signal of gene 7 of Agrobacterium T-DNA"
         .;
0
                                                                                                                                                                                                                       PARP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "phosphinothricin acetyltransferase"
                                                                                                                                                                                                                       Transgenic plant; poly-(ADP-ribose) polymerase inhibitor;
niacinamide; Agrobacterium; T-DNA; male sterile; barnase;
ribonuclease; RNase; cereal; wheat; Triticum aestivum;
         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                  /note= "promoter region of rice El gene"
complement (4336..5710)
 Pred. No. 1.5e-29;
        1; Mismatches
                                                                                                                                                                                                                                                                                              complement (2019..2288)
                                                                                                                                                                                                                                                                                                                                                              complement (2625..4313)
                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                  Oryza sativa;
cauliflower mosaic virus.
                                                                                                                                                                                                                                                                                                                                                      /product= barnase
                                                                                                                                                            AAT61394 standard; DNA; 6548 BP
                                                                                                                                                                                                                                                                                                     /*tag= a
/label= 3'nos
                                                                                                                                                                                                                                                                                                                                                                                                          P35S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= 3'g7
99.08;
                                                                                                                                                                                                                                                         Chimeric Agrobacterium sp.;
Chimeric Oryza sativa;
Chimeric cauliflower mosaic
                                                                                                                                                                                                                                                                                                                                                                                                                                              /label- Bar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95EP-0401844
                                                                                                                                                                                                                                                                                                                                                                             /label- PE1
                                                                                                                                                                                                                                                                                                                                                                                                                                                            6243..6496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "3'
                                                                                                                                                                                                                                                                                                                                                                                                                              5711..6262
                                                                                                                                                                                          07-MAY-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= d
        Matches 190; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          /label-
                                                                                                                        6531 gaccatgtacgt 6542
                                                                                                           gaccatgtacat 192
Best Local Similarity
                                                                                                                                                                                                                                            plasmid pTS172; ds
                                                                                                                                                                                                        Plasmid pTS172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP757102-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-FEB-1997
                                                                                                                                                                            AAT61394;
                                                                                                                                                                                                                                                                                                                                                                                           promoter
                                                                                                                                                                                                                                                                                                                                                               promote
                                                                                                                                                                                                                                                                                       Key
3'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                            3'UTR
                                                                                                           181
                                                                                                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                      AAT61394
                                                                                                                                               RESULT
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plasmid pTS172 (AAT61394) contains the barnase coding sequence under control of the rice El gene stamen-specific promoter and a phosphinothricin acetyltransferase coding sequence under control of the cawn 35s promoter. Plasmid pTS172 and plasmid pTS772 (see also AAT61395) were used to transform wheat Spring variety Pavon calli via particle bombardment. Some calli were treated with the poly-(ADP-ribose) polymerase inhibitor niacinamide before, or before and after, bombardment. Healthy, male sterile plants were regenerated only from bombarded calli that were treated with niacinamide. This was believed to be due to more faithful expression characteristics of the integrated stamen-selective batnase gene in these callicated process. For plants transformed with pTS172, copies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6351 ctacggcaatgtaccagctgatataatcagttattgaaatatttctgaatttaaaacttgc 6410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ctacggcaatgtaccagctgatataatcagttattgaaatattctgaatttaaacttgc 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Male sterile plant; mutant barnase gene; anther-specific expression; low fidelity PCR; primer; plant breeding; ss.
                                                                                                                                                                                                                                                 Prodn. of transgenic plants using a poly-(ADP-ribose) polymerase inhibitor - reduces the cultured cells response to stress and \phantom{a}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 6548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6548 BP; 1756 A; 1579 C; 1523 G; 1690 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E. coli plasmid pTS172 containing synthetic barnase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 190; DB 18;
Pred. No. 1.5e-29;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                               Example 2; Page 17-20; 25pp; English
                                                              (PLBZ ) PLANT GENETIC SYSTEMS NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ91096 standard; DNA; 6548 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 99.0%;
Matches 190; Conservative 1
95EP-0401844.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6531 gaccatgtacgt 6542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 gaccatgtacat 192
                                                                                                                                                                                     WPI; 1997-111050/11.
                                                                                                                                                                                                                                                                                                                reduces metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200008176-A1.
04-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-FEB-2000
                                                                                                                          De Block M;
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misc_feature
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                 Hamada K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT39337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                promoter
                                                                                                                                                                                                                                                                                                                                                                                                                              12
                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 1
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                                                                                                                                                       The invention relates to the generation of male sterile plants by the introduction of a mutant barnase gene (AA291095) for expression specifically in the arther of a plant. This sequence represents the E. coll/Agrobacterium shuttle vector plasmid pTS172 which contains the synthetic barnase gene (AA291094) under control of the cauliflower mosaic virus 35s promover. The vector also contains a region of the Agrobacterium T-DNA gene 7. The vector is used for transmitting the barnase gene to plants via an Agrobacterium tumefaciens host cell. The transformed plant is used in plant breeding.
                                                                                               Mutate barnase gene for efficient construction of plant transformants, particularly male sterile plants free from any undesirable characters by specifically expressing the gene alone in anther
                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                1 ctacggcaatgtaccagctgatataatcagttattgaaatattctgaatttaaacttgc 60
                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                              Length 6548;
                                                                                                                                                                                                                                                           Sequence 6548 BP; 1756 A; 1579 C; 1523 G; 1690 T; 0 other;
                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Male sterile plant; RNAase inhibitor; plasmid pTS346;
                                                                                                                                                                                                                                                                                          Score 190; DB 21;
Pred. No. 1.5e-29;
1; Mismatches 1;
                                                                                                                                      Example 3; Page 19-23; 30pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF86441 standard; DNA; 7492 BP.
                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 99.0%;
Matches 190; Conservative
                   98JP-0220060
 99WO-JP04167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99JP-0279307
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                                      (NISB ) JAPAN TOBACCO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NISB ) JAPAN TOBACCO INC.
                                                           Nakakido F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6531 gaccatgtacgt 6542
                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 gaccatgtacat 192
                                                                             WPI; 2000-195581/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmid pTS346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200124616-A1.
03-AUG-1999;
                   04-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3T-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-APR-2001
                                                          Hamada K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAF86441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1
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plants. The method comprises inserting a promoter fragment upstream of an RNAse gene and a second promoter, upstream of an RNAse gene and inserting it into the plant genome. The method is useful for producing male sterile tobacco, lettuce and rapeseed plants, but preferably rice and maize. The present sequence is a vector used in the method of the present invention.
                                                                                                                                                                                                                                                                                                                                                                  tatttaaactatattttctttcaagatgggaattaacatctacaaattgccttttcttatc 180
                                                                                                                                     present invention relates to a method for producing male sterile
                                                                                                                                                                                                                                                                                                                                               Gaps
                                                           Method for producing male sterile rice and maize by inserting RNAse gene and RNAse inhibitor genes with promoters into the plant genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /function= 35S promoter of cauliflower mosaic virus strain CM1841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ds.
                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                               Length 7492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmid pTS88; male sterile; barstar; barnase; ribonuclease;
transqenic plant; rice; Oryza sativa; maize; corn; Zea mays;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= c
/label= barstar
/product= Bacillus amyloliquefaciens barstar
968..1287
/*tag= d
                                                                                                                                                                                                                                                          Sequence 7492 BP; 1987 A; 1801 C; 1752 G; 1952 T; 0 other;
                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                          Score 190; DB 22;
Pred. No. 1.5e-29;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= pgEM2
/note= "polylinker of pgEM2"
                                                                                                   Disclosure; Page 19-23; 29pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmid pTS88 (EcoRI-HindIII fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT39337 standard; DNA; 1303 BP
                                                                                                                                                                                                                                                                                                            45.7%;
99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= b
/label= P35s
                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 99.09
Matches 190; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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Nakakido F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7475 gaccatgtacgt 7486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gaccatgtacat 192
                              WPI; 2001-266212/27
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Synthetic.
                 deletion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH25423;
                                                                                                                                                                                                                                                              coding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
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                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                        jion containing polyadenylation signal gene 7 og Agrobacterium T-DNA
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                          The HindIII-EcoRI fragment (AAT39337) of plasmid pTS88 contains barstar DNA under control of a 35S promoter. The plasmid was used with PTS14 (see also AAT39336) contq. barnase DNA under control of the stamen-specific promoter El to produce male sterile rice cv. Kochihibiki transgenic plants, and with plasmid pVEI36 (see also AAT39338) contg. barnase DNA under control of the stamen-specific PCA55 promoter to produce male sterile maize plants. Expression of barnase (a ribonuclease) in the stamen leads to male sterility. Constitutive expression of barstar counteracts possible lqw level expression of barnase DNA in non-stamen tissue.
                                                                                                                                                                                              Prodn. of male sterile plants by transforming with a chimaeric construct - comprising a male sterility DNA e.g. barnase and a co-regulating gene, e.g. barstar, into the nuclear genome, useful for generating hybrid cultivars
                                                                                                                                                                                                                                                                                                                                                                                     ; DB 17; Length 1303;
.7e-29;
tes 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                           Sequence 1303 BP; 415 A; 287 C; 275 G; 326 T; 0 other;
                                                     PGEM2
                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      Score 189.6;
Pred. No. 1.7
                                                                                                                                                            Cornelissen M, Michiels F;
                                   /*tag= e
/label= pGEM2
/note= "polylinker of
          region
                                                                                                                                                                                                                                          Example 1; Page 38; 56pp; English
                                                                                                                                           GENETIC SYSTEMS NV
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                   oŧ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pPS029 Bt ICP coding sequence
                                                                                                                                                                                                                                                                                                                                                                                      45.6%;
/label= 3'q7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA; 3201
                                                                                                        96WO-EP00722
                                                                                                                          95EP-0400364
         /function=
                          1288..1303
                                                                                                                                                                                                                                                                                                                                                                                                       Matches 189; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1278 gaccatgtac 1287
                                                                                                                                                                              WPI; 1996-402373/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 gaccatgtac 190
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ14529 standard;
                                                                                                                                           (PLBZ ) PLANT
                          misc_feature
                                                                                                                                                             Botterman J,
                                                                                                        21-FEB-1996;
                                                                                                                          21-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-JAN-1992
                                                                                      29-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ14529
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ID AAQ1
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hybrid seed; male-sterility gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ctacggcaatgtaccagctgatataatcagttattgaaatattctgaatttaaacttgc 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "n" in the sequence refers to not known nucleotides. pPS029 is identical to pVE36 (AAQ15144), but carries both the aminoterminal modification and the internal modification of the Bt ICP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45.6%; Score 189.6; DB 12; Length 3201; illarity 99.5%; Pred. No. 1.8e-29; Conservative 1; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified Bacillus thuringiensis insecticidal crystal protein genes - having A and T sequences changed to G and C sequences encoding same amino acids, for increased expression levels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3201 BP; 880 A; 710 C; 720 G; 886 T; 5 other;
thuringiensis; insecticidal crystal protein;
                                                                                                                                                                                                                                                                                                                                                   Dockx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oilseed rape;
barstar gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleotide sequence of plasmid pTHW118
                                                                                                                                                                                                                                                                                                                                                   Stam M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 6(c); 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             See also AAQ14529, AAQ15142-44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH25423 standard; DNA; 4832
                                                                                                                                                                                                             91WO-EP00733
                                                                                                                                                                                                                                                                                                                                                   Cornelissen M, Soetaert P,
                                                                                                                                                                                                                                                       90EP-0401055
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                                                                                                                                                                                                                                                                                                     GENETIC SYST.
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                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1991-339820/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gaccatgtac 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 189; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sednence
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                                                                                                                                                                                                           17-APR-1991;
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misc_feature

misc_feature

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3'UTR

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misc_feature

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promoter

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3'UTR

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promoter

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08-DEC-1999;

De Both G,

14-JUN-2001

misc_feature

Key

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Location/Qualifiers
complement (1..25)
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AATS9531,C

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AATS9531;

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DY

O7-MAY-1997 (first entry)

XX

W

Transgenic plant; poly-(ADP-ribo

KW

Chimeric Agrobacterium sp.;

OS

Chimeric Arabidopsis thalians;

OS

Chimeric Arabidopsis thalians;

CS

Chimeric Arabidopsis thalians;

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Chimeric Arabidopsis thalians;

CS

Chimeric Nicotiana tabacum.

XX

Transgenic Modelen (97.

FT

Arabel RB

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Chimeric Arabidopsis thaliana;
Chimeric Nicotiana tabacum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 99.5%;
Matches 189; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 gaccatgtac 190
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"right border repeat from TL-DNA from pTiB6S3"
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small subunit gene from Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= p
/note= "left border repeat from TL-DNA from pTiB6S3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= j // fragment from 3' UTR of nopaline synthase gene from T-DNA of pring7 and containing plant polyadenylation signals"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "downstream of Bacillus amyloliquefaciens
barstar coding region"
complement (2981..3253)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= m
/note= "Barstar gene coding region from Bacillus
amyloliquefaciens"
complement (3254..4762)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= f
/*tag= f
/note= "synthetic polylinker derived sequences"
complement (331..882)
                                                                                                                                                                                                                                                                                                                                              /*tag= d
/note= "synthetic polylinker derived sequences"
complement (98..309)
                                                                                                                                                                          /*tag= b
_note= "synthetic polylinker derived sequences"
                                                                                                                                                                                                                                                   /*tag- c
/note- "residual sequence from TL-DNA at right
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= 1
/note= "synthetic polylinker derived sequences"
complement (2659, 2919)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "synthetic polylinker derived sequences"
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/note= "synthetic polylinker derived sequences"
4808..4832
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/note= "3' UTR from TL-DNA gene 7 of pTiB6S3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= g
/note= "Streptomyces hygroscopicus bialaphos
resistance (bar) gene"
complement (883..2608)
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/note= "anther-specific
                                                                                                                                                                                                                                                                                                       border repeat"
                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..2658
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                                                                                                                                                      26..53
/*tag=
                                                                                                                              'note-
                                                                                                                                                                                                                            54..90
/*tag=
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Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200141558-A1
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The specification describes a pair of transgenic winter oilseed rape plants suited for producing hybrid seed. One of the plants has an expression cassette comprising a male-sterility gene, and the other plant has an expression cassette comprising a fertility restorer gene, integrated into the genome. The fertility restorer gene is capable of preventing the activity of the male-sterility gene. The plant pair is seed have agronomic performance, genetic stability and adaptability to plasmid preventic backgrounds. The present sequence represents replanted plasmid plasmid comprises the barstar gene, which acts as a fertility restorer gene. The plasmid is used to create transgenic
Transgenic winter oilseed rape plants suited for producing hybrid seed with improved qualities, comprises a male-sterility gene and fertility restorer gene, integrated into the genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 tatttaaactatatttctttcaagatgggaattaacatctacaaattgcctttcttatc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transgenic plant; poly-(ADP-ribose) polymerase inhibitor; PARP; niacinamide; Agrobacterium; T-DNA; male sterile; barnase; ribonuclease; RNase; cereal; wheat; oilseed rape; Brassica napus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 189.6; DB 22; Length 4832;
Pred. No. 1.8e-29;
1; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4832 BP; 1528 A; 883 C; 932 G; 1488 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= RB
/note= "T-DNA right border"
complement (97..330)
                                                                                                                        Example 1; Page 80-82; 98pp; English
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plasmid pTHW107 is a vector carrying T-DNA (AAT59531) comprising a barnase coding sequence under control of the tobacco TA29 gene stamen-specific promoter and a phosphinothricin accepyltransferase coding sequence under control of an Arabidopsis Rubisco small subunit gene promoter. Oilseed rape hypocotyl explants were infected with Agrobacterium tumefaciens CS8CIRH carrying vector PTHW107 and helper Ti plasmid pW60. In some treatments, the hypocotyls were treated with the poly-(AAD-ribose) polymerase inhibitor niacinamide (250 mg/l) 4 days prior to infection. Plants regenerated from niacinamide-treated transformed calli expression profile of the transgenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prodn. of transgenic plants using a poly-(ADP-ribose) polymerase inhibitor - reduces the cultured cells response to stress and reduces metabolism
                                                                                          /note= "promoter region of Rubisco small subunit
gene of Arabidopsis thaliana"
complement (2658..3031)
                                                                                                                                                          /note= "3'untranslated region contg. the poly-A signal of the nopaline-synthase gene of Agrobacterium T-DNA"
                                                                                                                                                                                                                                                                                                   /note= "promoter region of tobacco TA29 gene"
complement (4822..4946)
                                        /product- phosphinothricin acetyltransferase complement (883..2608)
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                                                                                                                                                                                                                                                                                                                                                      /note= "T-DNA left border"
                                                                                                                                                                                                                                           /product= barnase
complement (3368..4876)
 complement (331..882)
/*tag= c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENETIC SYSTEMS NV
                                                                                                                                                                                                                   /*tag= f
/label= Barnase
                                                                                                                                                   nos
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/label= PTA29
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/label= PSSU
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/label= LB
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/label= 3'
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Gaps

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Query Match 45.6%; Score 189.6; DB 18; Length 4946; Best Local Similarity 99.5%; Pred. No. 1.8e-29; Matches 189; Conservative 1; Mismatches 0; Indels 0;

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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1472140 seqs, 8248589755 residues
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Listing first 45 summaries
                                                                                                                     OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	AX127757 Sequence	AX127755 Sequence	AX12//48 Sequence	E31991 Mutated bar	A60109 Sequence 2	A76916 Sequence 2	AR098308 Sequence	E31990 Mutated bar	144104 Sequence 23	AX172441 Sequence	A60108 Sequence 1	AR098307 Sequence	AX172440 Sequence	A71437 Sequence 7	ARO98311 Segmence	AX127748 Sequence	A24783 plasmid pps	ARV/4366 Sequence A24782 plasmid pJD	AR074387 Sequence	A10942 Nucleotide	Al0939 Nucleotide	AX172463 Sequence	144103 Sequence 22	AJZ51013 Transform	A18051 DNA used as	AR095107 Sequence	AR098313 Sequence	AXU12338 Sequence T49886 Segmence 2	I82374 Sequence 2	237515 Binary vect	X00431 Agrobacter1	X00493 Agrobacteri	E00404 Ti plasmid	16 D	Sol			15-MAY-2001						producing same				elite event MS-B2"
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ID	AX127757	AX127755	AX12//48	E31991	A60109	A76916	AR098308	E31990	I44104	AX172441	A60108	AR098307	AX172440	A71437	AB0112 AR098311	AX127748	A24783	A24782	AR074387	A10942	A10943	AX172463	144103		A18051	AR095107	AR098313	AX012338 T49886	182374		ATTDNA	ATACH5	E00404		AF 24 2861 ARGMTUB	ALIGNMENTS		DNA DNA WOOT 31042.		***			X 500 040	plants and	.0 03-MAY-2	Ξ.	/organism="synthetic cons	order flanking
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Best Local Similarity 99.5
Matches 192; Conservative
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/note="5' border flanking region of
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                                                                         DB 6;
1.4e-63;
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Pred. No. 3.7e-57;
1; Mismatches 3;
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# synthetic construct
artificial sequence.

| (bases 1 to 415)
Weston, B. and de Beuckeleer, M.
| Patent: WO 013104-A 8 03-MAY-2001;
Aventis CropScience N.V. (BE)
                                                                     99.9%; Score 415.6;
100.0%; Pred. No. 3.4
tive 0; Mismatches
                                        152
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Sequence 8 from Patent WO0131042.
AX127755
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/note="plant DNA"
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1. .193
/note="T-DNA"
194. .476
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/note="T-DNA"
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                                                                            Local Similarity 100.
hes 416; Conservative
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artificial sequence.
3E 1 (bases 1 to 5865)
RS Weston, B. and de Beuckeleer, M.
3 Male-sterile brassica plants and methods for producing same NAL Patent: WO 0131042-A 1 03-MAY-2001;
Aventis CropScience N.V. (BE)
Location/Qualifiers
source //organism="synthetic construct" //db_art="taxon:32630" //note="T-DNA of plasmid pcoll3" //note="T-DNA of plasmid pcoll3" //note="T-DNA of plasmid pcoll3" //note="T-DNA of plasmid pcoll3"
121 tatttaaactatatttctttcaagatgggaattaacatctacaaattgccttttcttatc 180
                                                                                                                  Gaps
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1; Mismatches 0;
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Sequence 1 from Patent WO0131042.
AX127748
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45.7%;
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1 (bases 1 to 6548)
De, B.M.
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Best Local Similarity 99.03
Matches 190; Conservative
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Plasmid PTS172
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C12N15/09,A01H5/00,C12N5/10,C12N9/22//(C12N5/10,C12R1:91), PC
                                                                                      synthetic construct.
synthetic construct
synthetic construct
a stificial sequence.
1 (bases 1 to 7599)
Hoffmann, B., Mollier, P. and Pelletier, G.
Promoter expressed specifically in the cells of plant roots,
recombinant vectors and host cells comprising same and transgenic plants obtained
Patent: WO 0100833-A 5 04-JAN-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (I.N.R.A.) (FR)
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Pred. No. 1.3e-24;
1; Mismatches 0; Indels
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Mutated barnase gene and transgenic plant thereof
Patent: JP 2000041682-A 4 15-FEB-2000;
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/db_xref="taxon:32630"
/db_xref="taxon:32630"
/ 1938 c 1937 g 1752 t
                                AX063413 7599 bp DNA
Sequence 5 from Patent WO0100833.
AX063413
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JP 2000041682-A/4
                                                                 AX063413.1 GI:12541201
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Best Local Similarity 99.5%;
Matches 192; Conservative 1
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unidentified.
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.ce 1..6539 / Continues / Organism='Escherichia coli LE392' Location/Qualifiers
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                                                                                                                                                     Length 6539;
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                                                                                                                                                    Score 190; DB 6;
Pred. No. 3.6e-24;
1; Mismatches 1;
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Sequence 2 from Patent W09706267.
A60109
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                                                                    /organism="unidentified"
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1579 c 1523 g 16
                                                                                  /db_xref="taxon:32644"
1578 c 1519 g 1
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KAZUYUKI HAMADA, FUMIO NAKAKIDO
C12N15/09,A01H5/00,C12N5/10,C12N9/22//(C12N5/10,C12R1:91), PC
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                                        121 tatttaaactatatttctttcaagatgggaattaacatctacaaattgccttttcttatc
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/organism='Escherichia coli LE392'
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Pred. No. 3.6e-24;
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Mutated barnase gene and transgenic plant thereof
Batent: J2000041682-A 3 15-FEB-2000;
JAPAN TOBACCO INC
OS Escherichia coli LE392
PN JP 2000041682-A/3
PD 15-FEB-2000
PF 04-AUG-1998 JP 1998220060
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/organism="unidentified"
/db_xref="taxon:32644"
a 1579 c 1523 g 1696
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JP 2000041682-A/3.
unidentified.
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Pred. No. 3.6e-24;
1; Mismatches 1; Indels
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Pred. No. 3.6e-24;
1; Mismatches 1; Indels
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Patent: US 6074876-A 2 13-JUN-2000;
                                              A/O916 6548 bp DNA circular PAT
Sequence 2 from Patent EP0757102.
A76916
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Sequence 2 from patent US 6074876.
AR099308
AR098308.1 GI:12807565
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1. .6548
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1 (bases 1 to 6548)
De, B.M.
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De Block, M.
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Matches 190; Conservative
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AR098308 LOCUS DEFINITION

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VERSION KEYWORDS SOURCE ORGANISM

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TITLE JOURNAL FEATURES

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                                                                                                                                                                                                                                                                           synthetic construct.
synthetic construct
artificial sequence.
[1] (bases 1 to 4832)
de Both, G. and de Beuckeleer, M.
Hybrid winter oilseed rape and methods for producing same Patent: WO 0141558-A 2 14-JUN-2001;
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="T-DNA of plasmid pTHW118"
1883...4065
/note="Hpal restriction fragment"
8 a 883 c 932 g 1488 t 1
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Pred. No. 4.3e-24;
1; Mismatches 0;
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Sequence 2 from Patent WO0141558.
AX172441
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Sequence 1 from Patent W09706267
A60108
A60108.1 GI:3715124
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Location/Qualifiers
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1 (bases 1 to 4946)
De, B.M.
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Matches 189; Conservative 1
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Cornelissen,M., Soetaert,P., Stam,M. and Dockx,J.
Modified Bacillus thuringlensis insecticidal-crystal protein genes and their expression in Dant cells
Patent: US 5633446-A 23 27-MAY-1997;
Location/Qualifiers
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Cornelissen,M., Reynaerts,A., Gossele,V. and Van Aarssen,R.
Marker gene
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99.5%; Pred. No. 4.5e-24;
tive 1; Mismatches 0;
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144104
                        AR078675 7811 bp DNA
Sequence 5 from patent US 5962768.
AR078675
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1. .7811
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1906 c 1873 g
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710 c 720 g
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Best Local Similarity 99.53
Matches 189; Conservative
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/organism="Transformation vector pTHW107"
/db_xref="taxon:126810"
a 891 c 963 g 1523 t
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PLANT GENETIC SYSTEMS NV (BE)
LOCALION/QUALIFIERS
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                                                                                         Query Match
45.6%; Score 189.6; DB 6;
Best Local Similarity 99.5%; Pred. No. 4.3e-24;
Matches 189; Conservative 1; Mismatches 0;
                   1. .4946
/organism="Transformation vector
/db_xref="taxon:126810"
a 891 c 963 g 1523 t
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45.6%; Score 189.6; DB 6;
Best Local Similarity 99.5%; Pred. No. 4.3e-24;
Matches 189; Conservative 1; Mismatches 0;
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Sequence 1 from Patent BP0757102.
A76915
PLANT GENETIC SYSTEMS NV (BE)
Location/Qualifiers
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Transformation vector pTHW107
artificial sequence; vectors.
1 (bases 1 to 4946)
De.B.M.
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A76915/c
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De Block,M.
Genetic transformation using a PARP inhibitor
Patent: US 6074876-A 1 13-JUN-2000;
Location/Qualifiers
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1; Mismatches 0;
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Sequence 13,
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/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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Copyright (c) 1993 - 2000 Compugen Ltd
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Listing first 45 summaries

    nucleic search, using sw model

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                                                                      Sequence 4,
Sequence 17,
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NAME/KEY: misc_feature
LOCATION: Complement((1)..(25))
OTHER INFORMATION: right border of Agrobacterium T-DNA (RB)
FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((98)..(330))
OTHER INFORMATION: region containing polyadenylation signal of gene
OTHER INFORMATION: of Agrobacterium T-DNA (3'97)
FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((331)..(882))
OTHER INFORMATION: region coding for phosphinothricin acetyl
OTHER INFORMATION: region coding for phosphinothricin acetyl
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OTHER INFORMATION: region containing polyadenylation signal of
OTHER INFORMATION: nopaline synthase gene of Agrobacterium T-DNA
OTHER INFORMATION: (3'nos)
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LOCATION: Complement((3032)..(3367))
OTHER INFORMATION: region coding for barnase of Bacillus
OTHER INFORMATION: amyloliquefaciens
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TITLE OF INVENTION: Method to obtain male sterile plants
FILE REFERENCE: NMSCOR
CURRENT APPLICATION NUMBER: US/08/894,440
CURRENT FILING DATE: 1997-11-12
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 4
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NAME/KEY: misc_feature
LOCATION: Complement((883)..(2608))
OTHER INFORMATION: promoter of small subunit gene of
OTHER INFORMATION: Arabidopsis (Pssu)
                                                           US-09-078-294-4
US-09-078-294-4
US-09-007-005-17
US-09-058-489-45
US-08-883-795A-36
US-08-883-795A-36
US-08-973-73-4
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US-08-973-73-4
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US-08-995-654-1
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INFORMATION: of nopaline synthase gene of Agrobacterium
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Patent No. 6074876
GENERAL INFORMATION:
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Best Local Similarity 99.08
Matches 190; Conservative
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LENGTH: 6548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 atcaataaawttatgtttttgcttggactataatacctgacttgttattttatcaataaa 120
                LOCATION: Complement((3168)..(4877))
OTHER INFORMATION: promoter of stamen-specific TA29 gene of Nicotiana
OTHER INFORMATION: tabacum (PTA29)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    '1 ctacggcaatgtaccagctgatataatcagttattgaaatattctgaatttaaacttgc 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: plasmid pTS174 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME.XET: misc_feature
LOCATION: Complement((2019)..(2283))
OTHER INFORMATION: 3' nos: region containing polyadenylation signal
                                                                                     NAME/KET: misc_feature
LOCATION: (4924)..(5216)
COTHER INFORMATION: promoter of nopaline synthase gene of
COTHER INFORMATION: Agrobacterium T-DNA (Phos)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (5217)..(5489)
COTHER INFORMATION: region coding for barstar of Bacillus
OTHER INFORMATION: amyloliquefaciens
FEATURE:
NAME/KEY: misc_feature
COTHER INFORMATION: region containing polyadenylation signal of contern INFORMATION: region containing polyadenylation signal of contern INFORMATION: of Agrobacterium T-DNA (3'97)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46.3%; Score 192.6; DB 3; Length 5864; 99.5%; Pred. No. 1,4e-35;
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| Petent No. 6025546
| GENERAL INFORMATION:
| APPLICANT: PLANT GENETIC SYSTEMS N.V.
| TITLE OF INVENTION: Method to obtain male sterile plants
| FILE REFERENCE: NMSCOR
| CURRENT APPLICATION NUMBER: US/08/894,440
| NUMBER OF SEQ ID NOS: 4
| SOFTWARE: Patentin Ver. 2.0
| LENGTH: 6548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 192.v,
Pred. No. 1.4e-35;
Pred. no. 1.4e-35;
                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((5840)..(5864))
OTHER INFORMATION: left border of Agrobacterium T-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (1)..(2003)
OTHER INFORMATION: pUC19 derived vector sequences
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5800 gaccatgtacatc 5812
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NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 192; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-894-440-4
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US-08-894-440-1
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121 tatttaaactatatttctttcaagatgggaattaacatctacaaattgccttttcttatc 180
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CTHER INFORMATION: region coding for phosphinothricin acetyl
OTHER INFORMATION: transferase (bar)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (6263)..(6496)
OTHER INFORMATION: region containing polyadenylation signal fo gene 7
US-08-894-440-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: plasmid PTS172 FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: (4336)...(5710)
OTHER INFORMATION: 355 promoter of Cauliflower Mosaic Virus (P35S)
FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                         gene of rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: DE BLOCK,
ARC
TITLE OF INVENTION: GENETIC TRANSFORMATION USING A PARP INHIBITOR
TITLE OF INVENTION: GENETIC TRANSFORMATION USING A PARP INHIBITOR
CURRENT APPLICATION NUMBER: US/08/817,188
CURRENT FILING DATE: 1997-05-15
EARLIER APPLICATION NUMBER: PCT/EP96/03366
EARLIER APPLICATION NUMBER: PP 95401844.6
EARLIER APPLICATION NUMBER: EP 95401844.6
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 6548;
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Pred. No. 5.7e-35;
1; Mismatches 1; Indels
LOCATION: Complement((2284)..(2624))
OTHER INFORMATION: region coding for barnase of Bacillus
OTHER INFORMATION: amyloliquefaciens
                                                                                           NAME/KEY: misc_feature
LOCATION: Complement((2625)..(4313))
OTHER INFORMATION: promoter of the stamen-specific El
OTHER INFORMATION: (PEI)
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/note= "the 3' end formation and polyadenylation region of T-DNA gene
CURRENT APPLICATION PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/549,680A
FILING DATE: 16 JANUARY 1996
CLASSIFICATION: 800
TTORNEY/AGENT TATA
NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 194..218
OTHER INFORMATION: /note= "T-DNA right border"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: complement (729..1340)
OTHER INFORMATION: /note= "the aac(6') coding
OTHER INFORMATION: sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COURTION: 3001.3023
CHER INFORMATION: /note= "T-DNA left border;
COTHER INFORMATION: sequences"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45.7%; Score 190; DB 2;
illarity 99.0%; Pred. No. 5.8e-35;
Conservative 1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_recomb
LOCATION: 1..7811
OTHER INFORMATION: /label= vector pTRVA3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: promoter
LOCATION: 1341..1756
OTHER INFORMATION: /label= 35S promoter
                                                                                                                                                                                    ATTORNEY/ACENT INFORMATION:
NAME: SVENSSON, LEONARD R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 2121-0111P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (synthetic)
                                                                                                                                                                                                                                                                                              (703) 205-8000
(703) 205-8050
                                                                                                                                                                                                                                                                                                                                   TELEX: 248345
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 7811 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 484..684
OTHER INFORMATION: /not
OTHER INFORMATION: poly
                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 gaccatgtacat 192
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Best Local Similarity
Matches 190; Conserv
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                                                                                                                                                                                                                                                                                                TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : LOCATION: (6263)..(6496)
: OTHER INFORMATION: 3'97: 3' untranslated region containing the OTHER INFORMATION: polyadenylation signal of gene 7 of Agrobacterium US-08-817-188-2
                                                           LOCATION: Complement((2019)...(2288))
OTHER INFORMATION: 3' nos: 3' untranslated region containing the OTHER INFORMATION: polyadenylation signal of the nopaline synthase OTHER INFORMATION: gene of Agrobacterium T-DNA.
                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
COCATION: (4336)..(5170)
OTHER INFORMATION: P35S: 35S promoter region of Cauliflower Mosaic
OTHER INFORMATION: VITUR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: bar: region coding for phosphinotricin
OTHER INFORMATION: acetyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: CORNELISSEN, MARCUS
APPLICANT: CORNELISSEN, MARCUS
APPLICANT: CORNELISSEN, VERONIQUE
APPLICANT: GOSSELE, VERONIQUE
APPLICANT: VAN AARSSEN, ROEL
TITLE OF INVENTION: MARKER GENE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: BITCH, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747
CITY: Falls Church
STREET: Virginia
COUNTRY: USA
ZIP: 22040-0747
                                                                                                                                                                                                                                                                                                  gene of
                                                                                                                                                                                      LOCATION: Complement((2289)..(2624))
OTHER INFORMATION: barnase: region coding for barnase
                                                                                                                                                                                                                                                                                              Ε1
                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: Complement((2625)..(4313))
OTHER INFORMATION: PE1: promoter region of
                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: Complement((5711)..(6262))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-549-680A-5/c; Sequence 5, Application US/08549680A; Patent No. 5962768; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 99.0
Matches 190; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6531 gaccatgtacgt 6542
                                                                                                                                               FEATURE: NAME/KEY: misc_feature
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ö 121 tatttaaactatatttctttcaagatgggaattaacatctacaaattgccttttcttatc 180 1 ctacggcaatgtaccagctgatataatcagttattgaaatatttctgaatttaaacttgc 60 ;

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TITLE OF INVENTION: MODIFIED BACILLUS THURINGIENSIS
TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
TITLE OF INVENTION: IN PLANT CELLS
TUBBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                     ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: George Mason Bldg., Washington & Prince Sts. CITY: Alexandria STATE: Vicquia COUNTRY: United States ZIP: 22313-1404 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/453,104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
45.6%; Score 189.6; DB 1; Length;
Best Local Similarity 99.5%; Pred. No. 6.5e-35;
Matches 189; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
1.CCATION: 2078..2082
OTHER INFORMATION: /note- "Nucleotides 2078-2082
OTHER INFORMATION: wherein N is not known."
US-08-453-104-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Rea, Teresa S
REGISTRATION NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 010830-032
RELECHONE: (703) 836-6620
TELEPHONE: (703) 836-620
INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,869
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: GB 90401055.0
FILING DATE: 18-APR-1990
ATTORNEY_AGENT_INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 23, Application US/08694824
; Patent No. 5877306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 3200 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3132 GACCATGTAC 3141
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US-08-694-824-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (968)..(1287)
OTHER INFORMATION: region containing polyadenylation signal of gene 7
OTHER INFORMATION: of Agrobacterium T-DNA (3'97)
                                                                                                                                                                                                                                                                                                                                        1 Sequence: HindIII-EcoRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KET: misc_feature
LCCATION: (36)..(694)
OTHER INFORMATION: 35S promoter of Cauliflower Mosaic Virus strain
OTHER INFORMATION: CM1841 (P35S)
FEATURE:
NAME/KET: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
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45.6%; Score 189.6; DB 3; Length 1303;
Best Local Similarity 99.5%; Pred. No. 6e.35;
Matches 189; Conservative 1; Mismatches 0; Indels 0;
Sequence 2, Application US/08894440
| Patent No. 6025546
| GENERAL INFORMATION:
| TITLE OF INVENTION: Method to obtain male sterile plants FILE REFERENCE: NSCOR
| CURRENT APPLICATION NUMBER: US/08/894,440
| CURRENT FILING DATE: 1997-11-12
| NUMBER OF SEQ ID NOS: 4
| SOFTWARE: Patentin Ver. 2.0
| LENGTH: 1303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (695)..(967)
OTHER INFORMATION: region coding for barstar of Bacillus
OTHER INFORMATION: amyloliquefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (1)..(35)
OTHER INFORMATION: POLYLINKER Of PGEM2 (PGEM2)
                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificate OTHER INFORMATION: fragment of p7888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: misc_feature
; LOCATION: (1288)..(1303)
COHER INFORMATION: polylinker of pGEM2
US-08-894-440-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
US-08-453-104-23
US-08-453-104-23
Sequence 23, Application US/08453104
Patent No. 5633446
CENERAL INFORMATION:
APPLICANT: CORNELISSEN, MATC
APPLICANT: STAM, MAIKe
APPLICANT: STAM, MAIKe
                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
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FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((97)..(330))
OTHER INFORMATION: 3'97: 3' untranslated region containing the
OTHER INFORMATION: polyadenylation signal of gene 7 of Agrobacterium
OTHER INFORMATION: T-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             small subunit gene of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: Complement((2658)..(3031))
OTHER INFORMATION: 3' nos: 3' untranslated region containing the
OTHER INFORMATION: polyadenylation signal of the nopaline synthase
OTHER INFORMATION: gene of Agrobacterium T-DNA
                                                                                   GENERAL INFORMATION:
APPLICANT: DE BLOCK, MARC
TITLE OF INVENTION: GENETIC TRANSFORMATION USING A PARP INHIBITOR
FILE REPERENCE: 2121-0127P
CURRENT APPLICATION NUMBER: US/08/617,188
CURRENT PILING DATE: 1997-05-15
EARLIER APPLICATION NUMBER: POTYEP96/03366
EARLIER FILING DATE: 1996-07-31
EARLIER FILING DATE: 1995-08-04
NUMBER: OF SEQ ID NOS: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: misc_feature
NAME/KEY: misc_feature
LOCATION: Complement((331)..(882))
COTHER INFORMATION: bar: region coding for phosphinotricin acetyl
OTHER INFORMATION: transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: T-DNA of OTHER INFORMATION: plasmid pTHW107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45.6%; Score 189.6; DB 3;
99.5%; Pred. No. 6.8e-35;
tive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATLON: Complement((483)..(2608))
THER INFORMATION: promoter region of Rubisco
OTHER INFORMATION: Arabidopsis thaliana (PSSU)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: Complement((4922)..(4946))
OTHER INFORMATION: LB: T-DNA left border
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: Complement((1)..(25))
OTHER INFORMATION: T-DNA right border
                                            Sequence 1, Application US/08817188
Patent No. 6074876
                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 99.5
Matches 189; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: Complement(()
                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 4946
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                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                    APPLICANT: SOCRABET, PICT
APPLICANT: STAM, MAINE
APPLICANT: STAM, MAINE
APPLICANT: STAM, MAINE
TITLE OF INVENTION: MODIFIED BACILLUS THURINGIENSIS
TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
TITLE OF INVENTION: IN PLANT CELLS
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                               ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: /note= "Nucleotides 2078-2082; OTHER INFORMATION: wherein N is not known." US-08-694-824-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/694,824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 189.6; DB 2;
Pred. No. 6.5e-35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/694,824
FILING DATE: 09-AUG-1996
CLASSIFFCATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,869
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: GB 90401055.0
FILING DATE: 18-APR-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RECISTRATION NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 010830-032
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (703) 836-650
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                      CORNELISSEN, Marc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 99.5%;
Matches 189; Conservative
                                                                                                                                                                                                                                                                                                    STATE: Virginia
COUNTRY: United States
ZIP: 22313-140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 3200 base pairs
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LOCATION: 2078..2082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                         CORRESPONDENCE ADDRESS ADDRESSE: Burns, Do
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
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GENERAL INFORMATION:
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LOCATION: Complement((3368)..(4876))
OCHER INFORMATION: PTA.29; promoter region of TA29 gene of Nicotiana
OTHER INFORMATION: tabacum
                                                                                                                                                                                                                                                                                                 DB 3; Length 4946;
LOCATION: Complement((3032)..(3367))
OTHER INFORMATION: barnase: region coding for barnase
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                                                                          atcaataaawttatgttttgcttggactataatacctgacttgttattttatcaataaa 120
                    GENERAL INFORMATION:
APPLICANT: DE BLOCK, MARC
TITLE COPINVENTION:
FILE REFERENCE: 2121-0127P
CURRENT APPLICATION NUMBER: US/08/817,188
CURRENT PILING DATE: 1997-05-15
EARLIER APPLICATION NUMBER: PCT/EP96/03366
EARLIER FILING DATE: 1996-07-31
EARLIER FILING DATE: 1996-07-31
SERLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PATENTIN VOET: 2.0
SEQ ID NO 5: 5
LENGTH: 5560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(25)
COCHER INFORMATION: pT18653
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LOCATION: (2765)..(3058)
OTHER INFORMATION: 3' untranslated region of the CaMV 35S transcript
OTHER INFORMATION: containing polyadenylation signals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (84)..(296)
OTHER INFORMATION: 3' 97: 3' untranslated region containing the
OTHER INFORMATION: polyadenylation signal of gene 7 of Agrobacterium
OTHER INFORMATION: T-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (4483)..(4671)
OTHER INFORMATION: IV2: region corresponding to the second intron of
OTHER INFORMATION: the ST-LSI gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (830)..(2760)
OTHER INFORMATION: pSSU: promoter region of Rubisco small subunit
OTHER INFORMATION: gene of Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: T-DNA of OTHER INFORMATION: plasmid pTHM142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: (3059)..(5056)
OTHER INFORMATION: uidA: region coding for beta-glucuronidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (318)..(869)
OTHER INFORMATION: bar: region coding for phosphinotricin
OTHER INFORMATION: acetyltransferase
                                                                                                                                                                                                                                                                                               Sequence 5, Application US/08817188 Patent No. 6074876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
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Gaps
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                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature

COTHER INFORMATION: (5059)

OTHER INFORMATION: nucleotides)

FEATURE:
NAME/KEY: misc_feature

COTHER INFORMATION: nucleotides)

MAME/KEY: misc_feature

COTHER INFORMATION: region with unknown sequence (may contain up to 2: COTHER INFORMATION: nucleotides)

OTHER INFORMATION: nucleotides)

MAME/KEY: misc_feature

LOCATION: (5476)...(5479)

OTHER INFORMATION: region with unknown sequence (may contain up to 2: COTHER INFORMATION: region with unknown sequence (may contain up to 2: COTHER INFORMATION: region with unknown sequence (may contain up to 2: COTHER INFORMATION: nucleotides)
                                                                                                               NAME/KEY: misc_feature
LOCATION: (5533)..(5560)
OTHER INFORMATION: LB: left border sequence of octopine TL-DNA from
OTHER INFORMATION: pTIB6S3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: CORNELISSEN, MATC
APPLICANT: SOETAERT, Piet
APPLICANT: STAM, Maike
APPLICANT: DOCKX, Jan
APPLICANT: VAN AARSSEN, Roel
TITLE OF INVENTION: MODIFIED GENES AND THEIR EXPRESSION IN
UNMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: BUINS "STAMPS OF STAMPS OF ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3; Length 5560;
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LOCATION: (5067)..(5502)
OTHER INFORMATION: P35S: 35S promoter region of CaMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Virginia—
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
45.6%; Score 189.6; DB 3;
Best Local Similarity 99.5%; Pred. No. 6.9e-35;
Matches 189; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
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Patent No. 595254
GENERAL INFORMATION:
APPLICANT: CORNELISSEN, Marc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 gaccatgtac 190
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/note= "Coding region of a truncated bt2 (cryIAb) gene, also designated as the bt884
                                                                                                                                1881 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC 1940
                                           MODIFIED GENES AND THEIR EXPRESSION IN PLANT CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,016
FILING DATE: 03-NOV-1994
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FF 91402920.2
FILING DATE: 30-OCT-1991
PRIOR APPLICATION NUMBER: GB 92400820.4
FILING DATE: 25-MAR-1992
ATTORNEX/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: plasmid DNA designated as pJD884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: McGowan, Malcolm K
REGISTRATION NUMBER: P39,300
REFERENCE/DOCKET NUMBER: 010830-049
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 22, Application US/08232016 Patent No. 5952547 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORNELISSEN, Marc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: SOETAERT, Plet
APPLICANT: STAM, Maike
APPLICANT: DOCKX, Jan
APPLICANT: VAN AARSSEN, Roel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 7639 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: MC
TITLE OF INVENTION: PL
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      circular
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                          2061 GACCATGTAC 2070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Alexandria STATE: Virginia
                                                                                                                                                                                                                              181 gaccatgtac 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                      JS-08-232-016-22
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                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 1793..2026
PTHER INFORMATION: /note= "3' regulatory sequence
OTHER INFORMATION: containing the polyadenylation site derived from Agrobacteriu
OTHER INFORMATION: T-DNA gene 7."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 3582..4407
UNTER INFORMATION: /note= "3' regulatory sequence
OTHER INFORMATION: containing the polyadenylation site derived from Agrobacteriu
OTHER INFORMATION: T-DNA octopine synthase gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Coding region of a truncated modified bt2 (cryIAb) gene, also designated as the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 7071..7566
OTHER INFORMATION: /note= "TR1' and TR2 promoter
OTHER INFORMATION: derived from Agrobacterium T-DNA (with modified leader with
OTHER INFORMATION: respect to sequence of pJD884 of SEQ ID NO. 22."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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LOCATION: 5600..6457
COCATION: 5600..6457
OTHER INFORMATION: /note= "Sequence complementary to
Patent No. 5952947
OTHER INFORMATION: the coding sequence of the beta-lactamase gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 2922..3581
OTHER INFORMATION: /note= "Coding sequence of
OTHER INFORMATION: chloramphenicol acetyl transferase gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 7566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
COGATION: 2396.2921
OTHER INFORMATION: defined from Cauliflower mosaic virus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 189.6; DB 2;
Pred. No. 7.1e-35;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: plasmid DNA designated as pPS0212
                                                                                                                                                                                                 NAME: MCGOWAN, MAICOLM K
REGISTRATION NUMBER: P39,300
REFERENCE/DOCKET NUMBER: 010830-049
TELECOMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 7566 base pairs
              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91402920.2
FILING DATE: 30-CCT-1991
PRIOR APPLICATION NUMBER: GB 92400820.4
APPLICATION NUMBER: GB 92400820.4
FILING DATE: 25-WAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: crylab6 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45.6%;
03-NOV-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 1.1785
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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LOCATION:
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NAME/KEY: misc_feature

1 ctacggcaatgtaccagctgatataatcagttattgaaatatttctgaatttaaacttgc 60

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NAME/KEY: misc_feature
LOCATION: Complement((98)..(330))
OTHER INFORMATION: region containing polyadenylation signal of gene 7
OTHER INFORMATION: of Agrobacterium T-DNA (3'97)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: Complement((883)..(2608))
OTHER INFORMATION: promoter of small subunit gene of Rubisco of OTHER INFORMATION: Arabidopsis (Pssu)
OTHER INFORMATION: Arabidopsis (Pssu)
FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((2559)..(3031))
OTHER INFORMATION: region containing polyadenylation signal of OTHER INFORMATION: (3'nos)
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                                                                                                                                                                                                                                                                                                           LOCATION: Complement((331)..(882))
OTHER INFORMATION: region coding for phosphinothricin acetyl
OTHER INFORMATION: transferase (bar)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
45.2%; Score 188; DB 3; Length 5864;
Best Local Similarity 98.9%; Pred. No. 1.6e-34;
Matches 188; Conservative 1; Mismatches 1; Indels
                                                                            NAME/KEY: misc_feature
LOCATION: Complement((1)..(25))
OTHER INFORMATION: right border of Agrobacterium T-DNA (RB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (5490)..(5765)
OTHER INFORMATION: region containing polyadenylation signal
OTHER INFORMATION: of Agrobacterium T-DNA (3'97)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KRET: misc_feature
LOCATION: Complement((3368)..(4877))
OTHER INFORMATION: promoter of stamen-specific TA29 gene
OTHER INFORMATION: tabacum (PTA29)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: (5217)...(5489)
OTHER INFORMATION: region coding for barstar of Bacillus
OTHER INFORMATION: amyloliquefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus
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LOCATION: (4924)..(5216)
OTHER INFORMATION: promoter of nopaline synthase gene
OTHER INFORMATION: Agrobacterium T-DNA (Pnos)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: Complement((5840)..(5864))
; OTHER INFORMATION: left border of Agrobacterium T-DNA US-08-894-440-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: Complement((3032)..(3367))
OTHER INFORMATION: region coding for barnase of
OTHER INFORMATION: amyloliquefaciens
                                  OTHER INFORMATION: plasmid pTC0113
                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: Complement(()
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                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: misc_feature
LOCATION: 3666.4491
OTHER INFORMATION: /note= "3' regulatory sequence
OTHER INFORMATION: containing the polyadenylation site derived from Agrobacteriu
OTHER INFORMATION: T-DNA octopine synthase gene."
                                         /note= "3' regulatory sequence
containing the polyadenylation site derived from Agrobacteriu
T-DNA gene 7."
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NAME/KEY: misc_feature
LOCATION: 5684..6541
OTHER INFORMATION: /note= "Sequence complementary to
Patent NO. 5952547
OTHER INFORMATION: the coding sequence of the beta-lactamase gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1965 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC 2024
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99.5%; Pred. No. 7.1e-35;
tive 1; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                      LOCATION: 3006.3665
OTHER INFORMATION: /note= "Coding sequence of OTHER INFORMATION: chloramphenicol acetyl transferase gene.
                                                                                                                                                     LOCATION: 2480_.3005
OTHER INFORMATION: /note= "355 promoter sequence
OTHER INFORMATION: derived from Cauliflower mosaic virus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
PERTURE:
OTHER INFORMATION: Description of Artificial Sequence: T-DNA of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature

1.0CATION: 7155..7639

2.0THER INFORMATION: /note= "TR1' and TR2' promoter

3.9CHER INFORMATION: derived from Agrobacterium T-DNA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: PLANT GENETIC SYSTEMS N.V.
TITLE OF INVENTION: Method to obtain male sterile plants
FILE REFERENCE: NMSCOR
CURRENT APPLICATION NUMBER: US/08/894,440
CURRENT FILING DATE: 1997-11-12
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 5864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08894440 Patent No. 6025546
OTHER INFORMATION: /not
OTHER INFORMATION: /not
OTHER INFORMATION: CONT
OTHER INFORMATION: T-DN:
                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 2480..3005
                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 99.5 Matches 189; Conservative
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NAME/KEY:
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APPLICANT: CORNELISSEN, Marc
APPLICANT: SOETAERT, Plet
APPLICANT: SOETAERT, Plet
APPLICANT: STAM, Maike
APPLICANT: STAM, Maike
APPLICANT: OCKX, Jan
TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
TITLE OF INVENTION: IN PLANT CELLS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
STREET: George Mason Bidg., Washington & Prince Sts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3025 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC 3084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ctacggcaatgtaccagctgatataatcagttattgaaatattctgaatttaaacttgc 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTHER INFORMATION: /note= "Nucleotides 2151-2155 OTHER INFORMATION: wherein N is not known." US-08-694-824-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/694,824
FILING DATE: 09-AGG-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 176.6; DB 2;
Pred. No. 5.7e-32;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSILICATION: 526
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,869
FILING DATE: 16-DE02
APPLICATION NUMBER: GB 90401055.0
FILING DATE: 18-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Rea, Teresa S
REGISTRATION NUMBER: 30,427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 010830-032 TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                        Sequence 22, Application US/08694824
Patent No. 5877306
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 3201 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature LOCATION: 2151..2155
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Best Local Similarity 99.4
Matches 176; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                              RESULT 14
JS-08-694-824-22
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                                                                                                                                                                                                         APPLICANT: CORNELISEN, Marc
APPLICANT: CORNELISEN, Marc
APPLICANT: SCETAERT, Piet
APPLICANT: STAM, Maike
APPLICANT: STAM, Maike
APPLICANT: DOCKY, Jan
TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
TITLE OF INVENTION: IN PLANT CELLS
TITLE OF INVENTION: IN PLANT CELLS
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bidg., Washington & Prince Sts.
CITY: Alexandria
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42.5%; Score 176.6; DB 1; Length 3201;
Best Local Similarity 99.4%; Pred. No. 5.7e-32;
Matches 176; Conservative 1; Mismatches 0; Indels 0;
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: LOCATION: 2151..2155

: OTHER INFORMATION: /note= "Nucleotides 2151-2155

: OTHER INFORMATION: wherein N is not known."

US-08-453-104-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,869
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: GB 90401055.0
FILING DATE: 18-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Rea, Teresa S
REGISTRATION NUMBER: 30,427
REGISTRATION NUMBER: 30,427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 010830-032
TELECOMMUNICATION INFORMATION:
TELEPHORE: (703) 836-6620
TELEFAK: (703) 836-5201
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWAKE: FATERITH RELEASE #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/453,104
                                                                                                                                                        Sequence 22, Application US/08453104
Patent No. 5633446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                  63 GACCATGTAC 54
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Cuery Match

Query Match

Best Local Similarity 99.3%; Pred. No. 1.4e-26;
Matches 152; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctacggcaatgtaccagctgatatatcagttattgaaatattctgaatttaaacttgc 60

Db 1033 CTACGGCAATGTACAGCTGATATAATCAGTTATTTTGAATTTTTGAATTTACC 1092

Qy 61 atcaataaawttatgtttttgcttggactataatacctgacttgttttttacaataa 120

Db 1093 ATCAATAAAATTTTTCTTTGTCTTGACTTGTTATTTTATCAATAA 1152

Qy 121 tatttaaactatttctttcaagatggaatt 153

Db 1153 TATTTAAACTATTTTCTTTCAAGATGGGAATT 1185

Search completed: December 19, 2001, 17:34:14
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at17b03.x AV193861 UI-M-BH1-AU068795 wb84b08.x

clone BA0 602386981 601896616 58291 MAR BB464829

zu45b04.r g166h07.x UI-M-AIO-

UI-M-AIO

AV670633 mq21b05.r xz99d05.x

we29a10.x EST270918

BB283443

Perfect score:

Sequence:

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Run

Scoring table:

Searched:

0B 0B

Minimum I Maximum I

Database

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Caenorhabditis elegans.

Caenorhabditis elegans

Caenorhabditis elegans

Eukaryota: Metazoa: Nematoda; Chromadorea; Rhabditida; Rhabditoidea

Eukaryota: Metazoa: Nematoda; Chromadorea; Rhabditida; Rhabditoidea

(bases 1 to 568)

(caenorhabditidae; Peloderinae; Caenorhabditis.

(caenorhabditidae; Peloderinae; Caenorhabditis.

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C26971 C26971 Rice
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AI880854 at17b03.x
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Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact jerome_reboul@dfci.harvard.edu or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HII74209 568 bp mRNA EST 09-JUL-2001 OSTFOJISPB.1 AD-WIMCDNA Caenorhabditis elegans cDNA similar to EXT 174209
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AW048935 U
AU068795 A
ALG69082 A
A1835705 U
AA47833 A
A1275018 G
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AV670633 A
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BB283443
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Dana Farber Cancer Institute
44 Binney Street, Boston, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 2425
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POLYA=No.
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AQ946406
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C26971
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AA124200
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KEYWORDS
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BG563856 602584663
AQ256131 nbxb0015D
AW370342 RC1-BT025
BE150747 RC1-HT026
BF589714 naa08h06.
AI562674 TENS2662
BE857550 7901606.x
H66110 yr70h02.r1
H66097 yr70e02.r1
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95.360 Million cell updates/sec
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            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
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/db_xref_"taxon:9606"
/db_xref_"taxon:9606"
/clone_lib="Human fetal heart, Lambda ZAP Express"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Euberia; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA090232 212 bp mRNA EST 24-OCT-1996 chp0019.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens AA090232 GI:1636716
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Liew CC
Department of Laboratory Medicine and Pathobiology
University of Toronto
Banting Institute, 100 College St., Toronto, Ontario, M5G1L5
                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                            Score 17.4; DB 11; Length 568;
Pred. No. 2.38+02;
0; Mismatches 1; Indels 0
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FORWARD: 5' GCCAAGCTCGAAATTAACCCTCACTAAAGGG 3'
BACKWARD: 5' CCAGTCAATTGTAATACGACTCACTATAGGGCG 3'
Seq primer: 5' GAAATTAACCCTCACTAAAGGG 3'
LOCALLOn/Qualifiers
/organism="Caenorhabditis elegans"
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90.0%; Pred. No. 3.8e+02;
tive 0; Mismatches 2;
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Unpublished (1996)
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94.7%;
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Fax: 4169785650
                                                                                                                                                                                                                                                                                          Best Local Similarity
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/lab_bost="DH10B (T1 phage-resistant)"
/note="Organ: liver: Vector: pDNR-LIB (Clontech); Site_1:
Sfil (ggcgcctcggcc); Site_2: Sfil (ggccattaggcc); Site_1:
Sfil (ggcgcctcggcc); Site_2: Sfil (ggccattaggcc); S and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-ATTCTAGAGGCCGACATGATGGCC] and 3' adaptor sequence:
5'-ATTCTAGAGGCCGACATGATGGCC] and 3' adaptor
sequence: 5'-ATTCTAGAGGCCGACATGATGATGGCG]
C, or G and N = A, C, G, or T). Average insert size 1:85
kb (range 1:0-4.0 kb). 15/15 colonies contained inserts
by PCR: This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
                                                                                                                                                         ò:
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
602584663F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4712630 5', BG563856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A GSS 23-OCT-1998
Library Oryza sativa genomic clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQ256131 700 bp DNA nbxb0015b03r CUGI Rice BAC L nbxb0015b03r, DNA sequence.
                                                                                       BG563856.1 GI:13571508
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AQ256131.1 GI:3780613
GSS.
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Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                 Homo sapiens
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Indels

1 ctacggcaatgtaccagctg 20

Best Local Similarity 90.09 Matches 18, Conservative

Length 212;

TITLE

COMMENT

REFERENCE AUTHORS source

FEATURES

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1. .170

/organism="Homo sapiens"
/db_aref="txxxxn:9606"
/dlone_lib="BP0255"
/dev_stage="Adult"
/dev_stage="Adult"
/note="Organ: breast, Vector: pucl8; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196
/716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

( hases 1 to 618)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagal,M.A., da Sliva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
                                                                                                              Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&t2=RC1-BT0255-
181099-012-f06&t3=1999-10-18&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 170.
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC1-HT0269-010
300-014-h02&t3=2000-03-01&t4=1)
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RC1-HF0269-010300-014-h02 HT0269 Homo sapiens cDNA, mRNA sequence.
BELSO747
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shotgun sequencing of the human transcriptome with ORF expressed
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Pred. No. 8.9e+02;
); Mismatches 0;
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100.0%; Pic
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Fax: +55-11-2707001
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Matches 16; Conserv
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MEDLINE
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BE150747
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/db_xrefe*taxon:4530"
/clone="hbxb0015D03r"
/clone="hbxb0015D03r"
/clone=lb="CGGI Rice BAC Library"
/tissue_type="Leaf"
/lab_nost="E. col1 BH10B"
/lab_nost="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
/note="Vector: pBeloBAC11; Site_1: HindIII; primary source
of troop of two most populated areas of the humld tropics
and subtropics, rely on rice as their primary source of
carbohydrate. Monocctyledonous rice is a diploid plant
(2n=24) with a haploid genome equivalent of 431 Mbp
(Arumquanthan and Earle, 1991). The relatively small
genome of rice, three times larger than that of
Arabidopsis, makes it suitable for genomic studies. In
order to facilitate positional cloning, physical mapping
and genome sequencing of rice, we have constructed a BAC
library from Oryas sativa, Nipponbare variety. The
library from Oryas sativa, Nipponbare variety. The
close coverage allows the isolation a particular sequence
with a probability of 99.9 %. Two high density filters,
each containing 18,432 clones (doubly spotted), represent
the whole library for colony screening."
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RC1-BT0255-181099-012-f06 BT0255 Homo sapiens CDNA, mRNA sequence.
AW370342
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Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 700)
Midy.R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)
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Pred. No. 7e+02;
0; Mismatches 1; Indels 0
                                                                                                                                          Context: Wing RA Clemson University Genomics Institute Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 7288 Fax: 864 656 4293 Email: rwing@clemson.edu Seg primer: GGAAACAGCTATGACCATG Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Oryza sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 152.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cultivar-"Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain-"Japonica"
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94.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 acggcaatgtaccagctg 20
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Best Local Similarity 94.4
Matches 17; Conservative
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BASE COUNT ORIGIN

DEFINITION

AW370342

RESULT

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ACCESSION VERSION KEYWORDS ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

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Gaps

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Matches 17; Conserv
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BE857550/c
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                                                                                                                                    /organism="Homo sapiens"
/db_xref='taxon:9606"
/dloxref='taxon:9606"
/clone_lib-"H70269"
/dev_stage="Addilf"
/note="Organ: head_neck; Vector: pucl8; Site_l: Smal;
Site_l: Smal; A mini-library was made by cloning products
derived from ORESTES POR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

27 a 121 c 106 g 164 t
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia: Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 325)

NOI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: Gapbs-rémail.nih.gov

Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CLOne distribution: NCI-CGAP Clone distribution information can be infoetimage llni.gov

Infoetimage llni.gov

Trace considered overall poor quality

Frace considered overall poor quality

Frace considered overall poor quality

High quality sequence stop: 1.

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//dev_atage="adult"
/lab_host="DH10B"
//note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI_CGAP_Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BF589714 325 bp mRNA EST 12-DEC-2000 naa08h06.x1 NOT_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3254267 3'similar to TR:099829 Q99829 COPINE I. ;, mRNA sequence.
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100.0%; Pred. No. 1.1e+03;
.1ve 0; Mismatches 0;
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/clone_lib="NCI_CGAP_Pr28"
Seq primer: puc 18 forward
High quality sequence start: 50
High quality sequence stop: 617.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="r. cruzi epimastigote normalized cDNA Library"
/cell_type="epimastigote"
/note="colnA library constructed with oligo dT primed
epimastigote mRNA and cloned in pt7t318D phagemid with
modified polylinker (PHARMACIA)" 6 others
reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 985608-986759, 1101192-1101959, and 1217928-1220615). Subtraction by Bento Soares and M. Fatima Bonaldo. "
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7g01f06.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3305219 3'
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Av. Gral Paz entre Albarellos Proceduologicas (Univ. Nac. de Gral
Av. Gral Paz entre Albarellos y Constituyentes, INTI edificio 24
Tel: (54-1)752-9639 or (54-1)752-9639
Fax: (54-1)752-0021 or (54-1)752-9639
Email: daanchezeinti.gov.ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum.
1 (bases 1 to 390)
Verdun, R.E., Di Paolo, N.C., Urmenyi, T.P., Rondinelli, E., Frasch, A.C.C. and Sanchez, D.O.
Gene discovery through expressed sequence tag sequencing in trypanosoma cruz!
Lrypanosoma cruz!
1099003155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Sanchez D.O.
Instituto de Investigaciones Biotecnologicas (Univ. Nac. de Gral
                                                                                                                                                                                                                                                                             Gaps
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Pred. No. 1.3e+03;
0; Mismatches 2;
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/strain="Cl-Brenner"
/db_xref="taxon:5693"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 433) Mahairas, G.C., Mallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                      In washo mark here. Bit Floyett
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
7e1: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
High quality sequence stops: 356
Source: IMAGE Consortium, LLNL
This clone is available royalty free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: M13RPl
High quality sequence stop: 356.
Location/Qualifiers
,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rklin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wolldmann,P. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQ438334 433 bp DNA GSS 31-MAR-1999 HS_5131_A1_C08_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate-707 Col=15 Row-E, DNA sequence.
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High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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Pred. No. 1.3e+03;
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A0438334.1 GI:4549673
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89.5%;
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Matches 17; Conservative
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GGAP Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
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yr70h02.rl Soares fetal liver spleen lNFLS Homo sapiens cDNA clone
IMAGE:210675 5' similar to gb:X69970_cds1 TYROSINE-PROTEIN KINASE
RYK (HUMAN);, mRNA sequence.
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NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI/NINDS-CGAP http://www.ncbi.nlm.gov/ncicgap.
NCI/NINDS-CGAP http://www.ncbi.nlm.gov/ncicgap.
CGAP/BTGAP), Tumor Gene Index
Unpublished (1988)
COntact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 433) Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  to TR: Q9VKF0 Q9VKF0 CG14939 PROTEIN. ;, mRNA sequence.
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Bonaldo, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      info@image.linl.gov
Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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/clone="IMAGE:3305219"
                                      BE857550.1 GI:10371688
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Duncy 20539644
Contact: Erika Asamizu
The First Laboratory for plant Gene Research
The First Laboratory for Chipa 202-0812, Japan
Kazusa Dha Research Institute
Yana 1532-3, Kisarazu, Chiba 202-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AV632594 Chlamydomonas reinhardtii 5% CO2 Chlamydomonas reinhardtii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Chlamydomonas reinhardtii 5% CO2"
/note="Vector: pBluescriptII SK'; Site_1: EcoRI; Site_2:
XhoI; The cDNA library was constructed from cells cultured
in a medium with bubbling air containing 5% carbon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chlamydomonas reinhardtii
Ebkaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
1 (bases 1 to 454)
Asamiacu, E., Mutra,K., Kucho,K., Inoue,Y., Fukuzawa,H., Ohyama,K.,
Generation of expressed sequence tags from low-CO2 and high-CO2
DMA. Res. 7 (5), 305-307 (2000)
                                                                                                                                                                                                                                                                                                                                            79.0%; Score 15.8; DB 11; Length 438; 89.5%; Pred. No. 1.3e+03; 1ve 0; Mismatches 2; Indels 0.
                                                                /clone_lib="Soares fetal liver spleen INFLS"
/sex="male"
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Pred. No. 1.3e+03;
0; Mismatches 2;
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               /db_xref="GDB:3783491"
                                 /db_xref="taxon:9606"
/clone="IMAGE:210650"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="C9"
/db_xref="taxon:3055"
/clone="HC010b05_r"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                      Email: jwallace@u.washington.edu
Glones are derived from the human BAC library RPCI-11. For BAC
Glones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
http://www.htsc.washington.edu
plate: 707 row: E column: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HD5097 438 bp mRNA EST 18-OCT-1995
YF70602.rl Soares fetal liver spleen INFLS Homo sapiens cDNA clone
IMAGE:210650 5' similar to gb:x69970_cds1 TYROSINE-PROTEIN KINASE
HG6097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
High quality sequence stops: 348
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 15.8; DB 13; Length 433;
Pred. No. 1.3e+03;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                          /clone="Plate=707 Col=15 Row=E"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
                                                                                                                                                                                                                         1.433
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                        High quality sequence stop: 433.
Location/Qualiflers
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/organism="Homo sapiens"
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High quality sequence stop: 348.
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89.5%;
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Email: 100) 616-3887
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RESULT 14 BF009521/c

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REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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1. .602
/organism="Trypanosoma brucei"
/strain="Trypanosoma brucei"
/strain="Trypanosoma brucei"
/db_xref="taxon:5691"
/clone="Sheared DNA-105B6"
/clone="Sheared DNA-105B6"
/clone="Sheared DNA-105B6"
/clone="Sheared DNA-105B6"
/clone="Sheared DNA-105B6"
/note="Vector: pUCIB: Site=1: Smal; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU9774 GUTat 10.1) was mechanically sheared to give a tight size distribution (approx 2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University press. 19491."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trypanosoma.

1 (bases 1 to 602)

1 El-Sayed, N., Zhao, H., Gill, S., Suh, E., Malek, J., Fujii, C., Gerrard, C., Leech, V., de Jong, P., Uilu, E., Meiville, S., Donelson, J., Fraser, C. and Adams, M.

Perser, C. and Adams, M.

Determination of clone end sequences from Trypanosoma brucei GUTat 10.1 sheared DNA library
Unpublished (1999)
Other, GSSs: Sheared DNA 10586.TF
Contact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Genomics
The Institute for Genomic Genomics
The Institute for Genomic Genomic Contact.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: nelsayed@tigr.org
Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
DNA library constructed at TIGR. Clones will be available for
distribution through Research Genetics, Alabama, USA. Sheared DNA
end sequences search page: http://www.tigr.org/tdb/mdb/tbdb/.
Seq primer: Ml3-Reverse
Class: shotgun
                                                                                                                                                                                                                                                                                                A2215252 602 bp DNA GSS 09-JUN-2000
Sheared DNA-105B6.TR Sheared DNA Trypanosoma brucei genomic clone
Sheared DNA-105B6, DNA sequence.
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Tel: 301 838 0200
Fax: 301 838 0208
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Pred. No. 1.3e+03;
0; Mismatches 2;
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Press, 1999)."
a 153 c 1
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AZ215252.1 GI:8432975
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Matches 17; Conservative
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Systems 1 to 472)

Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna A., Bolla, B., Marra, M., Hillier, L., Kudaba, T., Martin, J., Beck, C., Wylle, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers , Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk , R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann , R., Waterston, R. and Wilson, R.

AL, Materston, R. and Wilson, R.

Contact: Shoemaker R/Public Soybean EST Project
Unpublished (1999)

Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1800

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XhOI; The CDNA library was constructed from mRNA isolated
from the epicotyls of 2 week old seeding for the cultivar
Williams. The seedlings were germinated in a growth
chamber, excised above the soil level, and the plants
were placed in a 100 ppm solution of auxin for 24 hours
prior to harvesting. Complementary DNA was synthesized
from mRNA using a primer consisting of a poly(dr)
sequence with a XhoI restriction site. ECORI adapters
were ligated to the blunt-ended cDNA fragments followed
by XhoI digestion. The CDNA fragments were directionally
cloned into the ECORI-XhoI restriction site of the
pBluescript vector. The ligated cDNA fragments were
transformed into BHUB host cells (GibcobRL). This
                                                                                                                                                                                                                      BF009521 472 bp mRNA EST 06-OCT-2000
8891h03.yl Gm-c1064 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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/clone_lib="Gm-c1064"
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/dev_stage="2 week old"
/lab_host="DH10B"
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/cultivar="Williams"
/db_xref="taxon:3847"
                                                                                                                                                                                                                                                                                                    Gm-c1064-1518 5', mRNA sequence
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326 TACGCCATTTACCAGCTG 344
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Query Match

BASE COUNT ORIGIN

Plasmid DV130 comp

pvE36 Bt Plasmid D pPS029

Plasmid DV132 used Nucleotide sequenc T-DNA of plasmid p Nucleotide sequenc plasmid pTS172delt T-DNA of pTES4.

Plasmid pTCO113 T-Plasmid pTCO113 T-Plasmid pTCO113 T-Chimeric T-DNA of E. coll plasmid pT Plasmid pTS172. CE. coll plasmid pTS346. Uplasmid pTS346. Upl

Right flanking reg T-DNA right border PCR primer for the PCR primer MDB193 P3202 EcoR1 primer Human 5' EST isola

Nucleotide sequenc Human cDNA sequenc

Enterococcus faeca

Perfect score:

Sequence:

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Scoring table:

Searched:

Database

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Transgenic plant; winter oilseed rape; hybrid seed; male-sterility gene; fertility restorer gene; barnase gene; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transgenic winter oilseed rape plants suited for producing hybrid seed with improved qualities, comprises a male-sterility gene and fertility restorer gene, integrated into the genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCR primer for the right border in transgenic plant MS-BN1
                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                       AAZ29123
AAH25423
AAH26439
AAR86439
AAV39339
AAT39339
AAT39339
AAT39339
AAT39339
AAT39339
AAT39336
AAT61394
AAT61394
AAT61394
AAT61394
AAT6139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 4; Page 43; 98pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AVET ) AVENTIS CROPSCIENCE NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            De Beuckeleer M;
                                                                                                                                                                                                                                06-DEC-2000; 2000WO-EP12872.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0457037
                                                                                                                                                                                                                                                                                                                                                                                                             AAH25428 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                        7566
7599
7639
24593
24596
                    3333
3694
3894
44983
52946
5394
5396
6539
6539
6548
6548
                                                                                                                                                                                                                                          19
1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-381419/40.
WO200141558-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Both G,
15.8
15.8
15.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH25428;
                                                                                                                                                                                                                                                                                                                                                                                                    AAH25428
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                                                                                                                                                                                                                        0000
                                                                                                                                                                                                                                                                                                                                                                                                               PCR primer for the
PCR primer MDB258
Right (5') border
Left (3') border f
USP-Promoter-casse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Legumin-signalpept
USP-signalpeptide
USP-Promoter-casse
Chimeric neo gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid pTS88 (Eco
                                                                             (without alignments)
74.498 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                results predicted by chance to have a 1 to the score of the result being printed, of the total score distribution.
                                                                   Search time 230.16 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                               /SIDSB/gcgdata/geneseq/geneseqn/Na1980.DAT:*
/SIDSB/gcgdata/geneseq/geneseqn/Na1981.DAT:*
/SIDSB/gcgdata/geneseq/geneseqn/Na1982.DAT:*
/SIDSB/gcgdata/geneseq/geneseqn/Na1982.DAT:*
/SIDSB/gcgdata/geneseq/geneseqn/Na1983.DAT:*
/SIDSB/gcgdata/geneseq/geneseqn/Na1985.DAT:*
/SIDSB/gcgdata/geneseq/geneseqn/Na1986.DAT:*
/SIDSB/gcgdata/geneseq/geneseqn/Na1986.DAT:*
/SIDSB/gcgdata/geneseq/geneseqn/Na1988.DAT:*
/SIDSB/gcgdata/geneseq/geneseqn/Na1989.DAT:*
/SIDSB/gcgdata/geneseq/geneseqn/Na1989.DAT:*
/SIDSB/gcgdata/geneseq/geneseqn/Na1989.DAT:*
/SIDSB/gcgdata/geneseq/geneseqn/Na1989.DAT:*
/SIDSB/gcgdata/geneseq/geneseqn/Na1991.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                   /SIDS8/gcgdata/geneseq/geneseqn/MA1992.DAT:
/SIDS8/gcgdata/geneseq/geneseqn/NA1992.DAT:
/SIDS8/gcgdata/geneseq/geneseqn/NA1994.DAT:
/SIDS8/gcgdata/geneseq/geneseqn/NA1995.DAT:
/SIDS8/gcgdata/geneseq/geneseqn/NA1995.DAT:
/SIDS8/gcgdata/geneseq/geneseqn/NA1996.DAT:
/SIDS8/gcgdata/geneseq/geneseqn/NA1998.DAT:
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/SIDS8/gcgdata/geneseq/geneseqn/NA2000.DAT:
/SIDS8/gcgdata/geneseq/geneseqn/NA2000.DAT:
                                                                                                                                                                                                  1861242
          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                             930621 seqs, 428662619 residues
                                                                  December 19, 2001, 16:22:43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                               - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH25428
AAD06996
AAD06997
AAQ04705
AAQ04703
AAQ04704
AAQ04704
AAQ04704
AAQ25707
AAZ29122
                                                                                                                             ctacggcaatgtaccagctg 20
                                                                                                                                               IDENTITY_NUC Gapox 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of res
score greater than or equal to
and is derived by analysis of
                                                                                                   US-09-698-903B-7
20
                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                         N_Geneseq_1101:*
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415
415
1037
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Match
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Score

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us-09-698-903b-7.rng

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Gaps

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ö DB 22; 0.26;

Score 20; DB Pred. No. 0.20 ; Mismatches

/ Match 100.0%; Local Similarity 100.0%; les 20; Conservative 0

Query Match

Best Loc Matches

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Gaps

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; 0

0; Mismatches Score 20; Pred. No.

0.26;

DB 22; Length 20; Indels

.; 0

Length 20; Indels

BP; 5 A; 6 C; 5 G; 4 T; 0 other;

Sequence 20

X OS

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The specification describes a pair of transgenic winter oilseed rape bants as a suited for producing hybrid seed. One of the plants has an expression cassette comprising a male-sterility gene (e.g. barnase fertility restorer gene (e.g. barstar gene), integrated into the genome. The fartility restorer gene (e.g. barstar gene), integrated into the genome. The fartility restorer gene is capable of preventing the activity of the male-sterility gene. The plant pair is useful for producing hybrid seed. Plants developed from the hybrid seed have agronomic performance, genetic stability and adaptability to different genetic backgrounds. PCR primers AAH125427-28 were used to amplify the right border of a vector in a transgenic plant which carries the TA29-barnase
                                                                                                                                                                                                                                                                                                   Sequence 20 BP; 5 A; 6 C; 5 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ctacggcaatgtaccagctg 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-OCT-2000; 2000WO-EP10680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              De Beuckeleer M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ctacggcaatgtaccagctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-300517/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Agrobacterium sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200131042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-MAY-2001,
                                                                                                                                                                                                                                                            transgene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Weston B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAD06996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAIL; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD06996
ID AAD0
×88888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              윱
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PÇR primer MDB258 to generate the flanking region of elite event MS-B2. MS-B2 elite event; transgenic Brassica plant; transformation event; male-sterility gene; PCR primer; thermal asymmetric interlaced; Transgenic Brassica plants, seeds, cells or tissues, characterized harboring specific transformation events, particularly by presence male-sterility gene, at specific location in its genome -Example 3; Page 28; 53pp; English. (AVET) AVENTIS CROPSCIENCE NV AAD06996 standard; DNA; 20 BP. CCCCCCCCCXBXBXBXBXBXBXBXBXBXXBXBXXXXXXBXBXBXBXBX

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seed, cells or tissues, characterised by harbouring a specific transformation event, particularly by harbouring a specific certansformation event, particularly by the presence of a male-sterility gene, at a specific location in the Brassica genome. Transgenic transgenic plant is useful for producing a hybrid seed by crossing the transgenic plant with a male-fertile Brassica plant and harvesting the hybrid seed from the transgenic Brassica plant and harvesting the The present sequence is right (5') border flanking region of elite event
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ρλ
                                                                                                                            elite event; transgenic Brassica plant; transformation event;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transgenic Brassica plants, seeds, cells or tissues, characterized ) harboring specific transformation events, particularly by presence male-sterility gene, at specific location in its genome -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a transgenic Brassica plant
                                                                                                 Right (5') border flanking region of elite event MS-B2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 415 BP; 154 A; 55 C; 70 G; 136 T; 0 other;
                                                                                                                                                                                                                                 1..234
/*tag= a
/note="Corresponds to plant DNA"
235..415
                                                                                                                                                                                                                                                                                        /*tag= b
/note= "Corresponds to T-DNA"
                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; Page 51; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
≩
AAD06997/c
ID AAD06997 standard; DNA; 415
                                                                                                                                                                         - Agrobacterium sp.
- Brassica sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                (AVET ) AVENTIS CROPSCIENCE
                                                                                                                                                                                                                                                                                                                                                                                        26-OCT-2000; 2000WO-EP10680
                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0430497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            De Beuckeleer M;
                                                                     06-AUG-2001 (first entry)
                                                                                                                                           male-sterility gene; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-300517/31.
                                                                                                                                                                                                                                                                                                                                 WO200131042-A2
                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                   29-OCT-1999;
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                                           AAD06997;
                                                                                                                                                                                       Chimeric
                                                                                                                              MS-B2
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Gaps

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100.0%; Score 20; DB 22; Length 415; ilarity 100.0%; Pred. No. 0.38; Conservative 0; Mismatches 0; Indels

Query Match Best Local Similarity Matches 20; Conserv

The present invention relates to a transgenic Brassica plant or its seed, cells or tissues, characterised by harbouring a specific transformation event, particularly by the presence of a male-sterility gene, at a specific location in the Brassica genome. Transgenic Brassica plant is useful for producing a hybrid seed by crossing the transgenic plant with a male-fertile Brassica plant and harvesting the hybrid seed from the transgenic Brassica plant.

The present sequence is tertilary thermal interlaced (TAIL)-PCR primer WDB258 used to right (5') and left (3') border flanking region of elitement. WS-B2. This primer corresponds to position 224-243 of plasmid

AAD06999

ò g

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The unique BglII-Ort (720-725) site is for ligating foreign DNA and the HindIII-Ort in the 3' polylinker (1032-1037) for cloning the cassette in the Ti-vector pGA471. Agrobacterium tumefaciens is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         n DNA incorporation; recombinant DNA techniques; plant genome; legumin; B4 gene; signalpeptide; Le-Sig.T7.; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 20; DB 11; Length 1037; Pred. No. 0.43;
                                                                                                                                                                                                                                                                                                                                                                                            Incorporation of DNA into higher plant genome - by specified recombinant DNA techniques.
                                                                                                                                Foreign DNA incorporation; recombinant DNA techniques; higher plant genome; legumin; USP-Pr.T7-1; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1037 BP; 338 A; 174 C; 166 G; 359 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product=Legumin-signalpeptide
                                                                                                                                                                                                                                                                                                                                     Hai NV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lequmin-signalpeptide cassette Le-Sig.T7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                     X,
                                                                                                     USP-Promoter-cassette USP-Pr.T7.1
            BP.
                                                                                                                                                                                                                                                                                                                                     Baumlein H, Muntz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       841 ctacggcaatgtaccagctg 860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ04703 standard; DNA; 1085
           AAQ04705 standard; DNA; 1037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ctacggcaatgtaccagctg 20
                                                                                                                                                                                                                                          89DE-3920034
                                                                                                                                                                                                                                                                         88DD-0319887.
                                                                                                                                                                                                                                                                                                     (PFLA-) VE KOMB PFLANZENZUC
                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-OCT-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; ; pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   See also AAQ04703-Q04706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     747..814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag=
                                                                                                                                                                                                                                                                                                                                                                 WPI; 1990-172459/23
                                                                                                                                                                                                                                          20-JUN-1989;
                                                                                                                                                                                                                                                                         19-SEP-1988;
                                                                       12-OCT-1990
                                                                                                                                                                              DE3920034-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Foreign DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DE3920034-A
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                                                                                                                                                                                                            31-MAY-1990
                                                                                                                                                                                                                                                                                                                                     Bassuner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transfected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ04703;
                                          AAQ04705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          higher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
AAQ04705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a transgenic Brassica plant or its seed, cells or tissues, characterised by harbouring a specific transformation event, particularly by the presence of a male-sterility gene, at a specific location in the Brassica genome. Transgenic Brassica plant is useful for producing a hybrid seed by crossing the transgenic plant with a male-fertile Brassica plant and harvesting the hybrid seed from the transgenic Brassica plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transgenic Brassica plants, seeds, cells or tissues, characterized by harboring specific transformation events, particularly by presence of male-sterility gene, at specific location in its genome -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                          MS-B2 elite event; transgenic Brassica plant; transformation event;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 20; DB 22; Length 416; 100.0%; Pred. No. 0.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                            Left (3') border flanking region of elite event MS-B2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 416 BP; 137 A; 72 C; 54 G; 152 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                 /*tag= a
//note= "Corresponds to T-DNA"
194..416
/*tag= b
/note= "Corresponds to plant DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1..193
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Page 52; 53pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AVET ) AVENTIS CROPSCIENCE NV.
                                                                                                                     BP.
           1 ctacggcaatgtaccagctg 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - Agrobacterium sp.
- Brassica sp.
                                                                                                                  AAD06999 standard; DNA; 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-OCT-2000; 2000WO-EP10680.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              De Beuckeleer M;
                                                                                                                                                                             06-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                          male-sterillty gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-300517/31.
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                                                                                                                                                                                                                                                                                                                                             misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Weston B,
                                                                                                                                                                                                                                                                                     Chimeric
Chimeric
                                                                                                                                                AAD06999;
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Gaps

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Indels

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89DE-3920034

20-JUN-1989;

RESULT

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Gaps

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Indels

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The unique BglII-Ort (720-725) site is for ligating foreign DNA and HindIII-Ort in the 3' polylinker (1261-1266) for cloning the cassette in the Ti-vector pGA471. Agrobacterium tumefaciens is
              ligating foreign DNA and the HindIII-Ort in the 3' polylinker (1155-1160) for cloning the cassette in the Ti-vector pGA471. The cassette is cloned into the binary Ti-vectors pGA471 and Agrobacterium tumefaciens is transfected. See also AAQ04703-Q04706.
                                                                                                                                                                                              Score 20; DB 11; Length 1160;
Pred. No. 0.43;
Mismatches 0; Indels 0

    by specified

                                                                                                                                 Sequence 1160 BP; 369 A; 192 C; 188 G; 411 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Foreign DNA incorporation; recombinant DNA techniques; higher plant genome; legumin; USP-Pr.T7-2; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Incorporation of DNA into higher plant genome recombinant DNA techniques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hai NV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Baumlein H, Muntz K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USP-Promoter-cassette USP-Pr.T7.2.
                                                                                                                                                                                                                                                                                                                                                                                                                  BP
                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ25707 standard; DNA; 1186 BP.
                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  964 ctacggcaatgtaccagctg 983
                                                                                                                                                                                                                                                                      1 ctacggcaatgtaccagctg 20
                                                                                                                                                                                                                                                                                                                                                                                                         AAQ04704 standard; DNA; 1166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89DE-3920034.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; ; pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          See also AAQ04703-Q04706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1990-172459/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-JUN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-SEP-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DE3920034-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bassuner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAY-1990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transfected
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ04704;
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AAQ04704
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                8.588888
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                                                                                                                                                                                                                                                                                         for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                      The Legumin gene B4 is used. The unique BglII-Ort (815-820) site is ligating foreign DNA and the HindIII-Ort in the 3' polylinker (1080-1085) for cloning the cassette in the Ti-vector pGA471. The cassette is cloned into the binary Ti-vectors pGA471 and Agrobacterium tumefaciens is transfected.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 20; DB 11; Length 1085; 100.0%; Pred. No. 0.43; 0; Mismatches 0; Indels 0
                                                                                                                                                                      Incorporation of DNA into higher plant genome - by specified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Incorporation of DNA into higher plant genome - by specified recombinant DNA techniques.
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1085 BP; 368 A; 219 C; 155 G; 343 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Foreign DNA incorporation; recombinant DNA techniques; higher plant genome; signalpeptide; USP-Sig.T7.; ss.
                                                                                      Wobus U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mobus
                                                                                    Hai NV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hai NV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The unique BglII-Ort (890-895) site is for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
/product=signalpeptide
747..817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USP-signalpeptide cassette USP-Sig.T7.
                                                                                Muntz K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
708..877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bassuner R, Baumlein H, Muntz K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88DD-0319887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA004706 standard; DNA; 1160
                                      (PFLA-) VE KOMB PFLANZENZUC
                                                                                                                                                                                                    recombinant DNA techniques.
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                                                                                Baumlein H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                     Disclosure; ; pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; ; pp; German.
                                                                                                                  WPI; 1990-172459/23.
P-PSDB; AAR05198.
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P-PSDB; AAR05199.
19-SEP-1988;
                                                                             Bassuner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-OCT-1990
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                                                       Gaps
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                                   Length 1166;
                                                       Indels
     other;
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Sequence 1166 BP; 381 A; 208 C; 196 G; 381 T; 0
                               100.0%; Score 20; DB 11; 100.0%; Pred. No. 0.43;
                                                                                                                                                               AAQ25707;
                                                                                                                                 AAQ25707
ID AAQ2
XX
AC AAQ2
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region containing polyadenylation signal of gene 7 og Agrobacterium T-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The HindIII-ECORI fragment (AAT39337) of plasmid pTS88 contains barstar DNA under control of a 355 promoter. The plasmid was used with pTS174 (see also AAT39336) contg. barnase DNA under control of the stamen specific promoter El to produce male sterile rice cv. Kochihibiki transgenic plants, and with plasmid pVE136 (see also AAT39338) contg. barnase DNA under control of the stamenspecific PCA55 promoter to produce male sterile maize plants. Expression of barnase (a ribonuclease) in the stamen leads to male sterility. Constitutive expression of barstar counteracts possible
                                                                                                                                        Jorgan b
/Label= P35S
/function= 35S promoter of cauliflower mosaic virus
/function= Strain CM1841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prodn. of male sterile plants by transforming with a chimaeric construct - comperising a male sterility DNA e.g. barnase and a co-regulating gene, e.g. barstar, into the nuclear genome, useful for generating hybrid cultivars
transgenic plant; rice; Oryza sativa; maize; corn; Zea mays; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Pred. No. 0.44;
Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                       /product- Bacillus amyloliquefaciens barstar
968..1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            low level expression of barnase DNA in non-stamen tissue
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                                                                                                  /label= pgEM2
/note= "polylinker of pGEM2"
                                                                                                                                                                                                                                                                                                                                                                                             /note= "polylinker of pGEM2'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Michiels F;
                                                          Location/Qualifiers
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                                                                                                                                                                                                                            /*tag= c
/label= barstar
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100.0%;
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/label= pGEM2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cornelissen M,
                                                                                                                                                                                                                                                                                     /*tag= d
/label= 3'97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96WO-EP00722
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                                                                                                                                                                                                                                                                                                                   /function-
                                                                                                                                                                                                                                                                                                                                                1288..1303
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Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                ..694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PLBZ ) PLANT
                                                       Key
misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3otterman J,
                                                                                                                                                                                                                                                                       polyA_signal
                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                            WO9626283-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-FEB-1995;
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                            Synthetic
                                                                                                                                   promoter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Two transformed corn plants were analysed by means of Southern hybridisation. As a probe, a 1184 bp EcoRT-HindIII fragment derived from another plasmid was used. The sequence of that plasmid is given below. Results showed that at least a chimeric neo gene was
                                                                     Nicotiana tabacum; neomycine phosphotransferase; Agrobacterium; ss.
                                                                                                                                                                a
"sequence derived from tapetum specific
promoter of Nicotiana tabacum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transforming monocotyledonous plants e.g. cereals - comprises wounding and/or degrading cells of intact plant tissue or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 13; Length 1186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmid pTS88; male sterile; barstar; barnase; ribonuclease;
                                                                                                                                                                                                                                                                                  3' regulatory sequence contg. the polyadenylation site derived from Agrobacterium T-DNA gene 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                     /product- neomycine_phosphotransferase 791..1186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1186 BP; 244 A; 317 C; 325 G; 300 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 20; DB 13
100.0%; Pred. No. 0.44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid pTS88 (EcoRI-HindIII fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    integrated into the plant genomic DNA
                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 60; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PLBZ ) PLANT GENETIC SYSTEMS NV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        90EP-0403332
91EP-0401888
                                                                                                                                                                                                                                                                   /*tag= c
/note= "3'
            (first entry)
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                                          gene probe
                                                                                                                                                                /*tag=
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                                                                                                                                                                                                                            /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dhalluin K, Goebel E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             embryogenic callus
                                         Chimeric neo
                                                                                                                                                                                                                                                       misc_feature
            07-DEC-1992
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08-JUL-1991;
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                                                                                                  Synthetic
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                                                                                                                                                promoter
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ID AAT3
XX
AC AAT3
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DT 22-J
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KW Plas
                                                                                                                                 Key
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"n" in the sequence refers to not known nucleotides. pPSO29 is identical to pVE36 (AAQ15144), but carries both the aminoterminal modification and the internal modification of the Bt ICP
                                                                                                                                                                                                                                                                                                                                                                                                    Modified Bacillus thuringlensis insecticidal crystal protein genes - having A and T sequences changed to G and C sequences encoding same amino acids, for increased expression levels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 20; DB 12; Length 3201; 100.0%; Pred. No. 0.49; tive 0; Mismatches 0; Indels 0.
                                                               Bacillus thuringiensis; insecticidal crystal protein; ICP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus thuringiensis; insecticidal crystal protein; ICP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3201 BP; 880 A; 710 C; 720 G; 886 T; 5 other;
                                                                                                                                                                                                                                                                                                                                        Stam M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 6(c); 78pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      See also AAQ14529, AAQ15142-44.
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                              pPS029 Bt ICP coding sequence.
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                                                                                                                                                                                                                                                                                                (PLAN-) PLANT GENETIC SYST
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Best Local Similarity
Matches 20; Conserv
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                                                                                    deletion; ss
                                                                                                                                                                                                                           17-APR-1991;
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                                                                                                                                                      WO9116432-A
                                                                                                                                                                                         31-OCT-1991
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                                                                                                                      Synthetic.
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                                                                                                                                                         Transgenic seed; marker; aleurone-specific promoter; Plasmid DV131; GFP:NPTII fusion protein construct; L3/EGFP:NPTII/Tr7; maize R gene; expression cassette; maize L3 oleosin gene; chimeric gene; transgene; MGFP:NPTII translational fusion; Tr7 terminator; Luciferase gene; assay; Green fluorescent protein; GFP; gene fusion; selection; screening; expression; automated seed screening technique; screenable marker; transformant; embryogenic tissue; implementation; ds.
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                                                                                                                      Plasmid DV131 comprising L3/EGFP:NPIII/Tr7 expression cassette.
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               AA229122 standard; DNA; 3153 BP.
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Matches 20; Conservative
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AAZ29122
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25-NOV-1999
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                                                                                                          PPS029 (AAQ14529) is identical to pVE36, but carries both the amino-
terminal modification and the internal modification of the Bt ICP
                                                                                                                                                                                                                                  Gaps
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0
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                    Modified Bacillus thuringiensis insecticidal crystal protein genes - having A and T sequences changed to G and C sequences encoding same amino acids, for increased expression levels
                                                                                                                                                                                                       Query Match 100.0%; Score 20; DB 12; Length 3201; Best Local Similarity 100.0%; Pred. No. 0.49; Matches 20; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                      Sequence 3201 BP; 915 A; 651 C; 700 G; 930 T; 5 other;
                                                                                              sequence refers to not known nucleotides.
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                                                                      Disclosure; Fig 6(c); 78pp; English
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                                                                                                                                             See also AAQ14529, AAQ15142-44
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pPS029 (AAC
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The present DNA sequence is the plasmid DV133, comprising
L3/rACTI intron/RGFP:RPTITYT7, that is used in the generation of
L3/rACTI intron/RGFP:RPTITYT7, that is used in the generation of
GFP:RPTII fusion protein constructs. It contains an expression cassette
comprising, a promoter from the maize is oleosin gene, the rice actin in intron, the coding sequence of EGFP:RPTII translational fusion, excised
from DV126 and the TT terminator. This plasmid is used to carry a chimeric gene, comprising an aleutrone-specific promoter like is, that is operably linked to a gene encoding a screenable marker, like Green
C100 perably linked to a gene encoding a screenable marker, like Green
C20 perably linked to a gene encoding a screenable marker, like Green
C310w both selection and screening of transformants. The aleurone-specific promoters direct the expression of the marker genes in campropenic tissues, allowing selection and screening of transgenic seeds avoids the need for transgenic seeds. Screening of transgenic seeds avoids the need for growing and assaying of seeds for transgenes and allows implementation
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allow both selection and screening of transformants. The aleurone-specific promoters direct the expression of the marker genes in embryogenic tissues, allowing selection and screening of viable transgenic seeds. Screening of transgenic seeds avoids the need for growing and assaying of seeds for transgenes and allows implementation of automated seed screening techniques for the identification of
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of automated seed screening techniques for the identification of transgenic seeds.
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Result Query No. Score Match Length DB ID	20 100.0 20 6 20 100.0 20 6	20 100.0 249 12	5 20 100.0 416 6 20 100.0 831 1 7 20 100.0 878 1	20 100.0 1037 6 20 100.0 1085 6 20 100.0 1160 6	20 100.0 1160 6 20 100.0 1166 6 20 100 0 1186 6	20 100.0 1186 6 20 100.0 1186 6	20 100.0 1186 6 20 100.0 1186 6	20 100.0 1186 6 20 100.0 2476 12	20 20 100.0 3201 6 21 20 100.0 3236 12	C 22 20 100.0 4946 6 A5015 C 24 20 100.0 4946 6 A76915 C 25 20 100.0 4946 6 A76915 C 25 20 100.0 4946 6 A7093307	26 20 100.0 4946 6 27 20 100.0 5349 6	29 20 100.0 5550 6	20 100.0 5865 6 20 100.0 5865 6	20 100.0 6539 6 20 100.0 6548 6 20 100.0 6548 6	20 100.0 6548 6	20 100.0 4348 6 20 100.0 7566 6 20 100 0 7566 6	20 100.0 7599 6 20 100.0 7639 6	41 20 100.0 7639 6	43 20 100.0 /811 6 43 20 100.0 12095 12 44 20 100.0 24595 1	20 100.0 24595	ALIGNMENTS	poetit e 1	20 bp	Sequence 7 from Patent W00131042. AX127754	N AX127754.1 DS	SOURCE synthetic construct. ORGANISM synthetic construct		TITLE Male-sterile brassica plants and methods JOURNAL Patent: WO 0131042-A 7 03-MAY-2001; a Aventis CropScience N.V. (BE) rinted, FEATURES Location/Qualifiers
GenCore version 4.5	oyright (c) 1993 - 2000	nucleic - nucleic search, using sw model	December 19, 2001, 16:22:38; Search time 1631.12 (without alignments) 202.280 Million cell	US-09-698-903B-7		table: IDENTITY_NUC Gapext 1.0	1472140 segs, 8248589755 residues	number of hits satisfying chosen parameters: 2944280	DB seq length: 0 DB seq length: 2000000000	ost-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries		gb_ba:		5: 9b_pst: 6: 9b_pst: 7: gb.pst:			12: gb_sy: 13: qb_us:*				20: en_or:* 21: en_ov:* 22: en_or:*		25: em_ro:* 26: em_sts:*			31: em_htgo_inv:* 32: em_htgo_rod:* 33: em_htgo_him:*	em	두다.

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/note="theroretical fusion junction (24) with gene 7 of Ti
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="5' border flanking region of elite event MS-B2"
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synthetic construct
artificial sequence.
1 (bases 1 to 415)
Weston, B. and de Beuckeleer, M.
Male-sterile brassica plants and methods for producing same
Patent: Wo 0.131042.A 8 03-MAY-2001;
Aventis Cropscience N.V. (BE)
Location/Qualifiers
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Pred. No. 11;
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/note="beta-1-tubulin sequence"
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/note="puc 13 polylinker"
29. .35
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220. .225
/note="put.polyA signal"
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                                                                                                                                 plasmid"
173. .178
/note="put.polyA signal"
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Sequence 10 from Patent W00131042.
AX127757
AX127757.1 GI:14134404
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Sequence 8 from Patent WO0131042.
AX127755
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/note="plant DNA"
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/note="T-DNA"
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Location/Qualifiers
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synthetic construct
afulficial sequence.
1 (bases 1 to 249)
Guiltinan, M.J., Velten, J., Bustos, M.M., Cyr, R.J., Schell, J. and
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                                                                                                                                                                                                                                                                                                  synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 20)
de Both, 6. and de Beuckeleer, M.
Hybrid winter oilseed rape and methods for producing same Petent: WO 0141558-A 9 14-JUN-2001;
Aventis CropScience N.V. (BE)
Location/Qualifiers
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Query Match

Best Local Similarity 100.0%; Pred. No. 15;

Matches 20; Conservative 0; Mismatches 0; Indels
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Pred. No. 15;
Mismatches 0;
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/protein_id=^0.70A29084.1"
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/translation="AMAWASSNWSTDPPWS"
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/db_xref="taxon:32630"
/note="primer 258"

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    /organism="synthetic construct"
/db_xref="taxon:32630"

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Sequence 9 from Patent W00141558.
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/note="unknown gene (148 is 1st base in codon) (525 is 3rd
base in codon)"
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Agrobacterium tumefaciens gene encoding 'transcript 7' mRNA for a
protein with unknown function.
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/db_xref="taxon:32630"
/note="3' border flanking region of elite event MS-B2"
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synthetic construct
artificial sequence.
We shows 1 to 416)
We ston, B. and de Beuckeleer, M.
Wale-sterile brassica plants and methods for producing same Patent: WO 0131042-A 10 03-MAY-2001;
Aventls Cropscience N.V. (BE)
Location/Qualifiers
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Submitted (27-MAY-1983) to the EMBL/GenBank/DDBJ databases
Data kindly reviewed (27-MAY-1983) by Dhaese P.
Location/Qualifiers
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/strain="(octopine TL-DNA)"
/db_xref="taxon:358"
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/note="CG [1] revised CC
/citation=[1]
/citation=[2]
99. 101
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148. .528
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unidentified reading frame.
Agrobacterium tumefaciens.
Agrobacterium tumefaciens
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/note="plant DNA"
72 c 54
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2 (bases 76 to 100)
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/note="T-DNA"
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/db_xref="GI.3181"
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LYGKGSLSQRIHDTHLKFKEKEELSFTTIKPAEMKAQQSDLTYYVAIFQSNYFLCVSN
PERGFIRKTNRFLYPIVAHGSMS"
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Rhizobiaceae; Rhizobium.
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Agrobacterium tumefaciens crown gall tumor T-DNA from T1 (tumor
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/note="polyadenylation signal"
189 c 139 q 262 t
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Pred. No. 8.9;
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/db_xref="taxon:358"
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McPherson, J.C.
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plasmid.
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Best Local Similarity 100.
Matches 20; Conservative
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/note="sequence derived from tapetum specific promoter of
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Nucleotide sequence 3 from patent number DE3920034,
A10941 GI:492368
                                                                                                           Query Match
100.0%; Score 20; DB 6; Length 1160;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 20; Conservative 0; Mismatches 0; Indels
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Matches 20; Conservative 0; Mismatches 0; Indels
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/gene="neomycine phosphotransferase gene"
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/db_xref="taxon:32630"
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Location/Qualifiers
1. .1160
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/db_xref="texton:32644"
a 194 c 188 g 411
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Location/Qualifiers
1. 1166
//organism="unidentified"
//db_Arref="taxon:32644"
381 a 208 c 196 g 381
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Location/Qualifiers
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100.0%; Score 20; DB 6; Length 1037;

Bost Local Similarity 100.0%; Pred. No. 8.7;

Matches 20; Conservative 0; Mismatches 0; Indels
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Query Match

Bost Local Similarity 100.0%; Pred. No. 8.6;

Matches 20; Conservative 0; Mismatches 0; Indels
                   Nucleotide sequence 4 from patent number DE3920034. Al0942. 1 GI:492369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A10943 1160 bp DNA PAT 2
Nucleotide sequence 5 from patent number DE3920034.
A10943.1 GI:492370
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                                                                                                                                                   Patent: DE 3920034-A 4 31-MAY-1990;
Location/Qualifiers
1. 1037
/organism="unidentified"
/db_xref="taxon:32644"
338 a 174 c 166 g 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent: DE 3920034-A 1 31-MAY-1990;
Location/Qualifiers
1.1085
/organism="unidentified"
/db_aref="taxon:32644"
369 a 218 c 155 g 343
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                1037 bp
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1 (bases 1 to 1160)
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EHOGIAPAELFARLKARMPGGEDLVVTHGDACLPNIMVENGRESGFIDGGRLGVADR
YQDIALATRDIAEELGGEWADRFLVLYGIAAPDSQRIAFYRLLDEFF"
1055. .1186
/note="3" regulatory sequence containing the
polyadenylation site derived from agrobacterium T-DNA gene
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/protein_id="CaA01373.1"
/db_xref="GI:4529900"
/translation="NELQDEAARLSWLATTGVPCAAVLDVVTEAGRDWLLLGEVPGQD
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D'Halluin, K. and Gobel, E.
Process for transforming monocotyledonous plants
Patent: US 6074877-A 2 13-JUN-2000;
Location/Qualifiers
1. 1186
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D'Halluin,K. and Gobel,E.
Process for transforming monocotyledonous plants
Patent: US 6002070-A 2 14-DEC-1999;
Location/Qualifiers
1. 1186
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Sequence 2 from patent US 6002070.
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Sequence 2 from patent US 6074877.
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317 c 325 q
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1 317 c 325 g
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Matches 20; Conservative
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Matches 20, Conservative
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9. .790
//note="coding sequence of neomycine phosphotransferase" 791. .1186 //note="3' regulatory sequence containing the polyadenylation site derived from Agrobacterium T-DNA gene
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/note="sequence derived from tapetum specific promoter of
Nicotiana tabacum"
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     6; Length 1186;
                                     Indels
                                                                                                                                                                                                                                                                            synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 1186)
D'Halluin,K. and Goebel,E.D.
Process for transforming monocotyledonous plants
Patent: EP 0955371-A 2 10-NOV-1999;
PLANT GENETIC SYSTEMS NV (BE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .1186
/organism="synthetic construct"
/ba xref="taxon:32630"
/note="DNA used as probe for neo gene"
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Score 20; DB 6,
Pred. No. 8.5;
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Job time: 3911 sec
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Sequence 2 from Patent EP0955371.
AX012338
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   Query Match 100.
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Matches 20; Conservative
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ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: probe
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Sequence 7,
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/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
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/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-475-975-2
US-09-084-889-2
US-09-084-889-2
US-09-080-625-3
US-08-64-824-23
US-08-64-824-23
US-08-64-824-23
US-08-69-824-23
US-09-080-625-2
US-09-080-625-5
US-09-080-625-5
US-09-080-625-5
US-09-894-440-4
US-08-894-440-4
US-08-894-440-1
US-08-817-188-2
US-08-894-440-1
US-08-817-188-2
US-08-894-440-1
US-08-817-188-2
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US-08-724-814-18
US-08-335-865J-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                       - nucleic search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                            US-09-698-903B-7
20
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Match 1
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                                                                                                                                                                                                                                                                                                                                                                         Sequence:
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                                                                                                                                                                                 Run on:
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Sequence 7, Appli
Sequence 2, Appli
Sequence 41, Appl
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                                     Sequence
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                      US-08-726-3064-22
US-08-726-3064-22
US-08-116-942-21
US-08-118-905-15
US-08-483-232-15
US-08-483-140-15
US-08-910-041-15
US-09-328-474-15
US-09-328-474-15
US-09-100-546-15
US-09-577-758-15
US-09-577-758-15
US-09-577-758-15
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US-08-814-095-7
US-09-103-840A-2
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CORRESPONDENCE ADDRESS:
ADDRESSE: Burns, Doane, Swecker & Mathis
ADRESSE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
CITY: Alexandria
COUNTY: 01ited States
ZIP: 22313-1404
COMPUTER READABLE FORM:
WEDIUM TYPE: Rioppy disk
COMPUTER: PROPPY disk
COMPUTER: PROPPY GISK
COMPUTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/064,121
FILING DATE: 24-MAY-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 9040332.1
FILING DATE: 23-NOY-1990
PRIOR APPLICATION NUMBER: BP 91401888.2
APPLICATION NUMBER: EP 91401888.2
ATTORNEY/AGENT INFORMATION:
NAMME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 010830-043
TELECOMMUNICATION NUMBER: 36,113
                                                                                                                                                                                  APPLICANT: D'HALLOIN, KAThleen
APPLICANT: GOBEL, Elke
TITLE OF INVENTION: PROCESS FOR TRANSFORMING
TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
NUMBER OF SEQUENCES: 5
Sequence 2, Application US/08064121 Patent No. 5641664 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1186 base pairs
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STRANDEDNESS: double
TOPOLOGY: linear
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SEQUENCE CHARACTERISTICS:
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NAME/KEY: -
LOCATION: 186
OTHER INFORMATION: /label= 3'g7
OTHER INFORMATION: /note= "3' regulatory sequence containing the OTHER INFORMATION: polyadenylation site derived from Agrobacterium US-08-064-121-2
                                                                   /note= "sequence derived from tapetum specific promoter of Nicotiana tabacum"
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Query Match

Bost Local Similarity 100.0%; Pred. No. 0.16;

Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                            /label= NPTII
/note= "coding sequence of neomycine phosphotransferase gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENT NC-DOS/MS-DOS
SOFTWARE: PATENT NC-DOS/MS-DOS
SOFTWARE: PATENT NO NOTA:
APPLICATION NUMBER: US/08/478,015
FLING DATE: 0-JUN-1995
PRIOR APPLICATION NUMBER: EP 9040332.1
FILING DATE: 23-NOV-1990
PRIOR APPLICATION NUMBER: EP 91401888.2
FILING DATE: 23-NOV-1991
PRIOR APPLICATION NUMBER: EP 91401888.2
FILING DATE: 23-UN-1991
PRIOR APPLICATION NUMBER: US 08/064,121
FILING DATE: 23-UN-1993
ATTORNEY/AGENT INFORMATION:
NAME: MCGCOWAN, MALCOLM K.
REFERENCE/DOCKET NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 39,300
REFERENCE/TOCKET NUMBER: 39,300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08478015
Patent No. 5712135
GENERAL INFORMATION:
APPLICANT: GOBEL, Elke
TITLE OF INVENTION: PROCESS FOR TRANSFORMING
TITLE OF INVENTION: DONOCOTYLEDONOUS PLANTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. BOX 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
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NAME/KEY:
LOCATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
NAME/KEY: -
LOCATION: 1..8
OTHER INFORMATION:
OTHER INFORMATION:
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US-08-478-015-2
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LOCATION: 9..790
OTHER INFORMATION: /label- NPTII
OTHER INFORMATION: /note- "coding sequence of neomycine phosphotransferase ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: -
; LOCATION: 791..1186
; OTHER INFORMATION: /label= 3'g7
; OTHER INFORMATION: /note= "3' regulatory sequence containing the polyadenylat;
; OTHER INFORMATION: site derived from Agrobacterium T-DNA gene 7"
US-08-478-015-2
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Facent No. 6002070

GENERAL IMPORMATION:

APPLICANT: D'HALLININ, Kathleen

APPLICANT: COBEL, Elke

TITLE OF INVENTION: PROCESS FOR TRANSFORMING

TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Burns, Doane, Swecker & Mathis

STREET: George Mason Bldg., Washington & Prince Sts.

CITY: Alexandria

CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Virginia

COMPUTER VIrginia

ZIP: 2213-1404

EDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPATIBLE

COMPUTER: IBM PC COMPATIBLE

COMPOTER: IBM PC COMPATIBLE

COMPOTER: IBM PC COMPATIBLE

SOFTWARE: PATENTIN Release #1.0, Version #1.25

SOFTWARE: PATENTIN Release #1.0, Version #1.25

FILING DATE: 07-JUN-1995

FLING DATE: 07-JUN-1995

CLASSIFICATION NUMBER: US 08/064,121

APPLICATION NUMBER: US 08/064,121

FILING DATE: 24-MAY-1993

APPLICATION NUMBER: EP 90403332.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: EP 90403332.1
FILING DATE: 23-NOV-1990
PRION APPLICATION DATA:
APPLICATION NUMBER: EP 91401888.2
FILING DATE: 08-JUL-1991
ATTORNEX/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 1033 CTACGGCAAIGTACCAGCIG 1052
                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANT-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ctacggcaatgtaccagctg 20
LENGTH: 1186 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.03
Matches 20; Conservative
                                                                                                                                                                                                                                           NAME/KEY: -
LOCATION: 1..8
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                             ORGANISM: probe
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/note= "sequence derived from tapetum specific promoter of Nicotiana tabacum"
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/note- "coding sequence of neomycine
phosphotransferase gene"
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Fatent No. 6035346
GENERAL INFORMATION:
APPLICANT: PLANT GENETIC SYSTEMS N.V.
TITLE OF INVENTION: Method to obtain male sterile plants
FILE REPRENCE: NMSCOR
CURRENT APPLICATION NUMBER: US/08/894,440
CURRENT FILING DATE: 1997-11-12
NUMBER OF SEQ ID NOS: 4
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                                                     FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91401888.2
FILING DATE: 08-JUL-1991
ATTORNEY/AGENT INFORMATION:
                               08/064,121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ctacggcaatgtaccagetg 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 1303
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Matches 20; Conservative
   PRIOR APPLICATION DATA:
                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 1..8
OTHER INFORMATION:
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LOCATION: 9..790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: probe
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US-08-894-440-2
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/note= "3' regulatory sequence containing the
polyadenylation site derived from Agrobacterium
T-DNA gene 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "sequence derived from
tapetum specific promoter of Nicotiana tabacum"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= NPTII
/note= "coding sequence of neomycine
phosphotransferase gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: D'HALLUIN, KAthleen
APPLICANT: D'HALLUIN, KAthleen
APPLICANT: GOBEL, Elke
TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/084,889
                                                           010830-043
               REGISTRATION NUMBER: 36.113
REFERENCE/DOCKET NUMBER: 0108
TELECHONIC: (703) 836-5620
TELEPHONE: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1186 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09084889 Patent No. 6074877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1033 CTACGGCAATGTACCAGCTG 1052
Crane-Feury, Sharon E
                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ctacggcaatgtaccagctg 20
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COUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 100.0
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 791..1186
COTHER INFORMATION: /
OTHER INFORMATION: /
COTHER INFORMATION: p
COTHER INFORMATION: p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: -
LOCATION: 1..8
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: -
LOCATION: 9..790
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
ORGANISM: probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
US-09-084-889-2
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Gaps

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Indels

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                                                                                      Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 20; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Alexandria
CITY: Alexandria
STATE: Virginia
COUPTR: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 3200 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
; TOPOLOGY: linear
US-09-080-625-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: 11:
MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (968)..(1287)
OTHER INFORMATION: region containing polyadenylation signal of gene 7
OTHER INFORMATION: of Agrobacterium T-DNA (3'97)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                 NAME/KEY: misc_feature
LOCATION: (36)..(694)
OTHER INFORMATION: 35S promoter of Cauliflower Mosaic Virus strain
OTHER INFORMATION: CM1841 (P35S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%; Score 20; DB 3; Length 1303;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09080625
Patent No. 6307123
GENERAL INFORMATION:
APPLICANT: Kriz, Alan L.
APPLICANT: Kriz, Alan L.
APPLICANT: Spencer, T. Mitchael
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TRANSGENE TITLE OF INVENTION: DENTIFICATION
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold White & Durkee
STREET: P.O. BOX 4433
                                                                                                                                                                                                               LOCATION: (695)..(967)
OTHER INFORMATION: region coding for barstar of Bacillus
OTHER INFORMATION: amyloliquefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-FOS/MS-DOS
SOFWWARE: PATENTINE Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/080,625
                   LOCATION: (1)..(35)
OTHER INFORMATION: POLYLINKER of pGEM2 (pGEM2)
                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEF: misc_feature
LOCATION: (1288)..(1303)
GTHER INFORMATION: polylinker of pGEM2
US-08-894-440-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Henson, Robert E.
REGISTRATION NUMBER: P-42,628
REFERENCE/DOCKET NUMBER: DEKM:161
TELEPHONE: (512) 418-3000
TELEPHONE: (512) 418-3000
TELEPHONE: (512) 447-757
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
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EDNESS: double
  NAME/KEY: misc_feature
                                                                                                                                                                     FEATURE:
NAME/KEY: misc_feature
LOCATION: (695)..(967)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucled
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-080-625-3
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## Sequence 23. Application US/08453104

| Sequence 23. Application US/08453104
| Sequence 23. Application US/08453104
| Sequence 23. Application US/08453104
| Sequence 23. Application US/08453104
| Patent No. 5633446
| APPLICANT: CORNELISSEN, Marc APPLICANT: SOFTAER, Piet APPLICANT: SOFTAER, Piet APPLICANT: DOCKX, Jan TITLE OF INVENTION: MODIFIED BACILLUS THURINGIENSIS
| TITLE OF INVENTION: IN PICANT CELLS INVENTION: IN PLANT CELLS INVENTION: INVENTION: IN PLANT CELLS INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION
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Score 20; DB 4; Length 3153;
Pred. No. 0.18;
Mismatches 0; Indels
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Query Match

Best Local Similarity 100.0%; Pred. No. 0.18;

Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,104
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,869
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: GB 90401055.0
FILING DATE: 18-APR-1990
ATTORNEY, AGENT INFORMATION:
NAME: Rea, Teresa S
RECISTRATION NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 010830-032
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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APPLICANT: CORNELISSEN, Marc
APPLICANT: SOETAERT, Piet
APPLICANT: STAM, Maike
APPLICANT: DOCKY, Jan
APPLICANT: DOCKY, Jan
TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
                                                              APPLICANT: SOETAERT, Plet
APPLICANT: STAM, Maske
APPLICANT: STAM, Maske
TITLE OF INVENTION: MODIFIED BACILLUS THURINGIENSIS
TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
TITLE OF INVENTION: IN PLANT CELLS
CORRESPONDENCES: 23
CORRESPONDENCES: 23
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                                                                                                                                                                                                                                                    ADDRESSEE: Burns, Donne, Swecker & Mathis STREET: George Mason Bldg., Washington & Prince Sts. CITY. Alexandria STATE: Virginia COUWTRY: United States ZIP: 22313-1404
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC COMPATION SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 2151.2155
OTHER INFORMATION: /note= "Nucleotides 2151-2155
OTHER INFORMATION: wherein N is not known."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: 05 90401055.0
FILING DATE: 18-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Rea, Teresa S
REGISTRATION NUMBER: 010830-032
FELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-620
TELEPHONE: (703) 836-2021
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 3201 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-453-104-22
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                                                                                                                                                                                                                              APPLICANT: CORNELISSEN, Marc
APPLICANT: SCRAFAET, Piet
APPLICANT: STAM, Maike
APPLICANT: STAM, Maike
APPLICANT: STAM, Maike
APPLICANT: DOCKX, Jan
TITLE OF INVENTION: INSCITICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
TITLE OF INVENTION: IN PLANT CELLS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
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: LCCATION: 2078..2082

: OTHER INFORMATION: /note= "Nucleotides 2078-2082

: OTHER INFORMATION: wherein N is not known."

US-08-694-824-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/694,824
FILING DATE: 09 AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 09-AUG-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,869
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: GB 90401055.0
FILING DATE: 18-APP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Rea, Teresa S
REGISTRATION NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 010830-032
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Virginia
COUNTRY: United States
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                        Sequence 23, Application US/08694824; Patent No. 5877306; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 22, Application US/08453104
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TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 3200 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                   2952 CTACGGCAATGTACCAGCTG 2971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2952 CTACGGCAATGTACCAGCTG 2971
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ctacggcaatgtaccagctg 20
1 ctacggcaatgtaccagctg 20
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Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Alexandria STATE: Virginia
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US-08-453-104-22
                                                                                                             RESULT 8
US-08-694-824-23
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Query Match

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100.0%; Score 20; DB 4; Length 3336; 100.0%; Pred. No. 0.18; Live 0; Mismatches 0; Indels
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APPLICANT: KILS. Alan L.
APPLICANT: Spencer, T. Michael
TITLE OF INVENITON: METHODS AND COMPOSITIONS FOR TRANSGENE
TITLE OF INVENITON: IDENTIFICATION
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold White & Durkee
STREET: P.O. Box 4433
CITY: Houston
                       COMPUTER: IBM PC compatible
CORFATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,625
CILASSIPCATION:
NAME: Hanson, Robert E.
REGISTRATION NUMBER: DEKM:161
TELECOMUNICATION INFORMATION:
TELEPHONE: (512) 474-7577
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3336 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARRE: PATCHILIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,625
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NAME: Hanson, Robert E.
REGISTRATION NUMBER: P-42,628
REFERENCE/COCKET NUMBER: DEKM:161
TELEFOMNUMICATION INFORMATION:
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/09080625
Patent No. 6307123
GENERAL INFORMATION:
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Matches 20; Conservative
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LENGTH: 3694 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTR: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
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EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
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100.0%; Score 20; DB 2; Length 3201;
Bost Local Similarity 100.0%; Pred. No. 0.18;
Matches 20; Conservative 0; Mismatches 0; Indels
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Patent No. 6307123
GENERAL INFORMATION:
APPLICANT: Kriz, Alan L.
APPLICANT: Kriz, Alan L.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TRANSGENE TITLE OF INVENTION: IDENTIFICATION
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold White & Durkee
STREET: P.O. Box 4433
CONTY: Houston
                                                                                                ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: George Mason Bldg., Washington & Prince Sts. CITY: Alexandria STATE: Virginia STATE: United States 217: 22313-1404
                                                                                                                                                                                                                                                                          COMPUTER: TALALA TALALA MEDIUM TYPE: Floppy disk COMPOTER: TBM PC Competible COMPUTER: TBM PC COMPOTED: COMPOTER: TBM PC COMPOTED: COMPOTER: TBM PC COMPOTED: COMPOTED: TBM PC COMPOTED: C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3025 CTACGGCAATGTACCAGCTG 3044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ctacggcaatgtaccagetg 20
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TYPE: nucleic acid
STRANDEDNESS: single
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ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-09-080-625-2
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Gaps

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243 CTACGCCAATGTACCAGCTG 224
                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
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NAME/KEY: misc_feature
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Best Local Similarity
Matches 20; Conserv
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US-08-817-188-5/c
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APPLICANT: DE BLOCK, MARC
TITLE OF INVENTION: GENETIC TRANSFORMATION USING A PARP INHIBITOR
FILE REFERENCE: 2121-0127P
CURRENT APPLICATION NUMBER: US/08/817,188
CURRENT APPLICATION NUMBER: PCT/EP96/03366
EARLIER APPLICATION NUMBER: PCT/EP96/03366
EARLIER FILING DATE: 1996-07-31
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     DB 4; Length 3694;
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                                                                                                                                                                                                                                                APPLICANT: KIIZ, Alan L.
APPLICANT: KIIZ, Alan L.
APPLICANT: Spencer, T. Michael
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TRANSGENE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold White & Durkee
STREET: P.O. Box 4433
CITY: HOUSTON
                                      0; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,625
                                        Mismatches
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   Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: DEKM:161
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 474-7577
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                             RESULT 13
US-09-080-625-4
Sequence 4, Application US/09080625
Fatent No. 6307123
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATTAME: Hanson, FObert E.
REGISTRATION NUMBER: P-42,628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
US-08-817-188-1/c
Sequence 1, Application US/08817188
; Patent No. 6074876
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                                                                                            3220 CTACGGCAATGTACCAGCTG 3239
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 100.0%;
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LENGTH: 3877 base pairs
Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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Best Local Similarity
Matches 20; Conserva
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US-09-080-625-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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Gaps
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OTHER INFORMATION: 3'97: 3' untranslated region containing the
OTHER INFORMATION: polyadenylation signal of gene 7 of Agrobacterium
OTHER INFORMATION: T-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: Complement((3368)..(4876))
OTHER INFORMATION: PTA29: promoter region of TA29 gene of Nicotiana
OTHER INFORMATION: tabacum
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: Complement((883)..(2608))
OTHER INFORMATION: promoter region of Rubisco small subunit gene of
OTHER INFORMATION: Arabidopsis thaliana (PSSU)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: Complement((2658)..(3031))
OTHER INFORMATION: 3' nos: 3' untranslated region containing the
OTHER INFORMATION: polyadenylation signal of the nopaline synthase
OTHER INFORMATION: gene of Agrobacterium T-DNA
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APPLICANT: DE BLOCK, MARC
TITLE OF INVENTION: GENETIC TRANSFORMATION USING A PARP INHIBITOR
FILE REFERENCE: 2121-0127P
CURRENT PAPLICATION NUMBER: US/08/817,188
CURRENT FILING DATE: 1997-05-15
EARLIER APPLICATION NUMBER: PCT/EP96/03366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: Complement((331)..(882))
OTHER INFORMATION: bar: region coding for phosphinotricin acetyl
OTHER INFORMATION: transferase
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                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: T-DNA of OTHER INFORMATION: plasmid pTHW107
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LOCATION: Complement((3032)..(3367))
OTHER INFORMATION: barnase: region coding for barnase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3;
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                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: Complement((1)..(25))
OTHER INFORMATION: T-DNA right border (RB)
EARLIER APPLICATION NUMBER: EP 95401844.6
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 5
SSOTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 4946
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LOCATION: Complement((4922)..(4946))
COTHER INFORMATION: LB: T-DNA left border
US-08-817-188-1
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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: T-DNA of OTHER INFORMATION: plasmid pTHW142
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(25)
OTHER INFORMATION: RB: right border sequence of octopine TL-DNA from
                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: misc_feature
LOCATION: (84)...(296)
OTHER INFORMATION: 3' 97: 3' untranslated region containing the
OTHER INFORMATION: 02) yadenylation signal of gene 7 of Agrobacterium
OTHER INFORMATION: T-DNA
FEATURE:
NAME/KEY: misc_feature
LOCATION: (318)...(869)
OTHER INFORMATION: bar: region coding for phosphinotricin
OTHER INFORMATION: acetyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (2765)..(3058)
OTHER INFORMATION: 3' untranslated region of the CaMV 35S transcript
OTHER INFORMATION: containing polyadenylation signals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature; COATION: (5476)..(5476)..(5479); OTHER INFORMATION: region with unknown sequence (may contain up to 20 corner INFORMATION: nucleotides)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20
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LOCATION: (4483)..(4671)
OTHER INFORMATION: IV2: region corresponding to the second intron of
OTHER INFORMATION: the ST-LS1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (5533)..(5560)
OTHER INFORMATION: LB: left border sequence of octopine TL-DNA from
OTHER INFORMATION: pTIB6S3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ដ
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NAME/KEY: misc_feature
LOCATION: (830)..(2760)
OTHER INFORMATION: pSSU: promoter region of Rubisco small subunit
OTHER INFORMATION: gene of Arabidopsis thaliana
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LOCATION: (3059)..(5056)
OTHER INFORMATION: uidA: region coding for beta-glucuronidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (5058)..(5059)
OTHER INFORMATION: region with unknown sequence (may contain
OTHER INFORMATION: nucleotides)
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LOCATION: (5077)...(5078)
OTHER INFORMATION: region with unknown sequence (may contain
OTHER INFORMATION: nucleotides)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LCCATION: (5067)..(5502)
OTHER INFORMATION: P35S: 35S promoter region of CaMV
EARLIER FILING DATE: 1996-07-31
EARLIER APPLICATION NUMBER: EP 95401844.6
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PATENTIN VEr. 2.0
SEQ ID NO 5
LENGTH: 5560
                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
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